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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
On: Fri Nov 13 17:13:47 1998; MasPar time 13.94 Seconds
ular output not generated. 828.366 Million cell updates/sec

Title: >US-08-989-362-2
Description: (1-316) from US08989362.pap
Perfect Score: 2294
Sequence: 1 MRRASRDYGYKLSSEMGs.....LLDPDQDQTYFGAFKVQDID 316

Scoring table: PAM 150
Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 46.143; Variance 97.466; scale 0.473

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	174	7.6	278	2 A49266	fas ligand - rat	7.29e-11
2	175	7.6	281	2 JC2340	Fas ligand - human	5.11e-11
3	172	7.5	279	2 A53062	Fas ligand - mouse	1.48e-10
4	165	7.2	146	5 IALY	cd40 ligand extracell	1.74e-09
5	165	7.2	261	2 I53476	CD40 ligand - human	1.74e-09
6	162	7.1	261	2 S53090	CD40 ligand - bovine	4.94e-09
7	160	7.0	235	1 QWMSN	tumor necrosis factor	9.87e-09
8	152	6.6	234	2 A25451	tumor necrosis factor	1.52e-07
9	150	6.5	235	2 JU0029	tumor necrosis factor	3.00e-07
10	150	6.5	260	2 S21738	CD40 ligand - mouse	3.00e-07
11	145	6.3	235	2 I54490	tumor necrosis factor	1.60e-06
12	143	6.2	234	2 JQ1344	tumor necrosis factor	3.10e-06
13	141	6.1	146	5 ICDAB	Cd40 ligand complex w	6.00e-06
14	141	6.1	146	5 ICDAC	Cd40 ligand complex w	6.00e-06
15	141	6.1	146	5 ICDAA	Cd40 ligand complex w	6.00e-06
16	136	5.9	306	2 I49139	lymphotoxin-beta - mo	3.06e-05
17	134	5.8	193	2 S06192	tumor necrosis factor	5.84e-05
18	130	5.7	151	5 2TUNA	Tumor necrosis factor	2.09e-04
19	130	5.7	151	5 2TUNE	Tumor necrosis factor	2.09e-04
20	130	5.7	151	5 2TUNF	Tumor necrosis factor	2.09e-04
21	130	5.7	151	5 2TUNC	Tumor necrosis factor	2.09e-04
22	130	5.7	151	5 2TUNB	Tumor necrosis factor	2.09e-04
23	130	5.7	151	5 2TUNB	Tumor necrosis factor	2.09e-04

24	128	5.6	233	2 S11688	tumor necrosis factor	3.93e-04
25	126	5.5	233	1 QWHUN	tumor necrosis factor	7.35e-04
26	123	5.4	152	5 ITNFB	tumor necrosis factor	1.86e-03
27	123	5.4	152	5 ITNFC	tumor necrosis factor	1.86e-03
28	123	5.4	152	5 ITNFA	tumor necrosis factor	1.86e-03
29	123	5.4	185	2 S52715	tumor necrosis factor	1.86e-03
30	124	5.4	233	2 S13114	tumor necrosis factor	1.37e-03
31	123	5.4	233	2 S24642	tumor necrosis factor	1.86e-03
32	123	5.4	233	2 S22052	tumor necrosis factor	1.86e-03
33	125	5.4	234	2 JH0529	tumor necrosis factor	1.00e-03
34	122	5.3	144	5 ITNRA	tumor necrosis factor	2.54e-03
35	122	5.3	205	1 QWHUX	lymphotoxin alpha pre	2.54e-03
36	114	5.0	232	2 S12606	tumor necrosis factor	2.83e-02
37	111	4.8	244	2 A46066	lymphotoxin beta - hu	6.81e-02
38	107	4.7	202	2 E27303	tumor necrosis factor	2.13e-01
39	106	4.6	345	2 S12788	transcription factor	2.86e-01
40	106	4.6	963	2 S45167	chitin synthase (EC 2	2.86e-01
41	103	4.5	197	2 JH0309	tumor necrosis factor	6.63e-01
42	104	4.5	202	2 JN0869	tumor necrosis factor	5.02e-01
43	104	4.5	1091	2 S33596	protein-tyrosine kina	5.02e-01
44	100	4.4	264	2 A30582	MHC class II histocom	1.51e+00
45	100	4.4	473	2 A54691	octamer-binding prote	1.51e+00

ALIGNMENTS

RESULT 1
ENTRY A49266 #type complete
TITLE fas ligand - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-Sep-1997

ACCESSIONS A49266
REFERENCE A49266
#authors Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
#journal Cell (1993) 75:1169-1178
#title Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor family.

#accession A49266
#status preliminary
#molecule_type mRNA
#residues 1-278 #label SUD
#cross-references GB:U03470; NID:G440178; PID:G440179
KEYWORDS glycoprotein; transmembrane protein
SUMMARY #length 278 #molecular_weight 31140 #checksum 9586

Query Match 7.6%; Score 174; DB 2; Length 278;
Best Local Similarity 26.7%; Pred. No. 7.29e-11;
Matches 36; Conservative 38; Mismatches 53; Indels 8; Gaps 6;

Db	152	SRSIPLE-WEDTYGTALISGVKYGKGLVINEAGLYFVYSKVYFRGO-SCNSQP----	LSH 206
QY	178	SHKVTLSWYHDSRGWAKISNMTLSNGLRVNQDGFYLYANICFRHHTSGSVPTDYQLQ	237
Db	207	KVYM-R-NFKYPGDLVMEER-KKLNCTTGQIWAHSYLVGAVFNLTADHLYVNISQLS	263
QY	238	MYVWVTKSIKPSHNLKMGKSTKNSGSEFHFYSINVGFFKLRAGEEISIQVSNPSL	297
Db	264	INFEESKTFGLYKL 278	
QY	298	LDPDQDQTYFGAFKV 312	

RESULT 2	JC2340	#type complete
ENTRY	Fas ligand - human	
TITLE	#formal_name Homo sapiens #common_name man	
ORGANISM	20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 31-Oct-1997	
DATE	JC2340; S57565; I38554	
ACCESSIONS	JC2340	
REFERENCE	Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioaka, T.; Kasahara, A.; Fusamoto, H.; Kamada, T.	

[illegible]

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RESULT      5
ENTRY
TITLE      CD40 ligand - human
ALTERNATE_NAMES
ORGANISM   protein
DATE       #formal_name Homo sapiens #common_name man
          02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
          13-Mar-1998
ACCESSIONS I53476; S28017; JH0793; S26694; S28852; S25684; S30593
REFERENCE
#authors   Gauchat, J.
#journal   FEBS Lett. (1992) 315:259-266
#title     Human CD40-ligand: Molecular cloning, cellular distribution
           and regulation of expression by factors controlling IgE
           production.
#citations  #cross-references MUID:93138085
#accession I53476
           ##status preliminary; translated from GB/EMBL/DDBJ
           ##molecule_type mRNA
           ##residues 1-261 ##label RES
           ##cross-references GB:L07414; NID:g180123; PID:g180124
REFERENCE
#authors   Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny,
           N.J.; Braesch-Andersen, S.; Noelle, R.J.; Stamenkovic, I.;
           Ledbetter, J.A.; Aruffo, A.
#journal   EMBO J. (1992) 11:4313-4321
#title     The human T cell antigen gp39, a member of the TNF gene
           family, is a ligand for the CD40 receptor: expression of a
           soluble form of gp39 with B cell co-stimulatory activity.
#accession S28017
           ##molecule_type mRNA
           ##residues 1-261 ##label HOL
           ##cross-references EMBL:Z15017; NID:g38483; PID:g38484
REFERENCE
#authors   Spriggs, M.K.; Armitage, R.J.; Stroockbine, L.; Clifford,
           K.N.; Macduff, B.M.; Sato, T.A.; Maliszewski, C.R.;
           Fanslow, W.C.
#journal   J. Exp. Med. (1992) 176:1543-1550
#title     Recombinant human CD40 ligand stimulates B cell proliferation
           and immunoglobulin E secretion.
#accession JH0793
           ##molecule_type mRNA
           ##residues 1-261 ##label SPR
           ##cross-references GB:X67878; NID:g38411; PID:g38412
           ##experimental_source peripheral blood T-cell
REFERENCE
#authors   Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek,
           R.A.
#journal   Eur. J. Immunol. (1992) 22:3191-3194
#title     Cloning of TRAP, a ligand for CD40 on human T cells.
#accession S26694
           ##status preliminary
           ##molecule_type mRNA
           ##residues 1-261 ##label GRA
           ##cross-references EMBL:X68550; NID:g37269; PID:g37270
REFERENCE
#authors   Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jonotte,
           T.; Elson, G.; Bonnefoy, J.Y.
#journal   FEBS Lett. (1993) 315:259-266
#title     Human CD40-ligand: molecular cloning, cellular distribution
           and regulation of expression by factors controlling IgE
           production.
#accession S28852
           ##molecule_type mRNA
           ##residues 1-261 ##label GAU
           ##cross-references EMBL:L07414
           ##note the sequence from Fig. 3 is inconsistent with that from
           Fig. 2 in having 6-Gln
GENETICS
#gene      GDB:CD40LG; HGIM1; IMD3
           ##cross-references GDB:I20632; OMIM:308230

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#title Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis factor.

#cross-references MUID:88224564

#accession A22908

##molecule_type DNA

##residues 1-235 ##label SHI

##cross-references GB:M20155

REFERENCE

#authors Shakhov, A.N.; Nedospasov, S.A.

#journal Bioorg. Khim. (1987) 13:701-705

#title Molecular cloning of the genes coding for tumor necrosis

factors: complete nucleotide sequence of the genomic copy of TNF-alpha in mice.

#cross-references MUID:87298639

#accession S03791

##molecule_type DNA

##residues 1-235 ##label SHA

##cross-references GB:M38296; NID:g202087

##note article in Russian with English abstract

REFERENCE

#authors Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.;

Nedospasov, S.A.

#journal Nucleic Acids Res. (1987) 15:9083-9084

#title Nucleotide sequence of the murine TNF locus, including the

TNF-alpha-(tumor necrosis factor) and TNF-beta-

(lymphotoxin) genes.

#cross-references MUID:88067722

#accession A27303

##molecule_type DNA

##residues 1-235 ##label SEM

REFERENCE

#authors Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.;

Goeddel, D.V.

#journal Proc. Natl. Acad. Sci. U.S.A. (1985) 82:6060-6064

#title Cloning and expression in Escherichia coli of the cDNA for

murine tumor necrosis factor.

#cross-references MUID:85298296

#accession A25164

##molecule_type mRNA

##residues 1-235 ##label PEN

##cross-references GB:M11731; NID:g202084; PID:g202085

REFERENCE

#authors Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van

der Heyden, J.; Kawashima, E.; Chollet, A.; Tizard, R.; van

Heuverswyn, H.; van Vliet, A.; Ruysschaert, M.R.; Fiers, W.

#journal Nucleic Acids Res. (1985) 13:4417-4429

#title Molecular cloning of mouse tumour necrosis factor cDNA and

its eukaryotic expression.

#cross-references MUID:85242112

#accession A23127

##molecule_type mRNA

##residues 1-235 ##label FRA

##cross-references GB:X02611; NID:g54844; PID:g54845

REFERENCE

#authors Cseh, K.; Beutler, B.

#journal J. Biol. Chem. (1989) 264:16256-16260

#title Alternative cleavage of the cachectin/tumor necrosis factor

propeptide results in a larger, inactive form of secreted

protein.

#cross-references MUID:89380231

#accession A34251

##molecule_type protein

##residues 70-87 ##label CSE

REFERENCE

#authors Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer,

S.L.; Cerami, A.

#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:1670-1674

#title Identification of a common nucleotide sequence in the

3'-untranslated region of mRNA molecules specifying

inflammatory mediators.

#cross-references MUID:86149365

#accession I59058

##status preliminary; translated from GB/EMBL/DBJ

##molecule_type mRNA

##residues 1-230, R', 232-235 ##label RES

##cross-references GB:M13049; NID:g202082; PID:g202083

REFERENCE

#authors Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.

#journal Biochem. Biophys. Res. Commun. (1990) 173:1072-1078

#title Characterization of high molecular weight glycosylated forms of murine tumor necrosis factor.

#cross-references MUID:91097531

#accession A36696

##molecule_type protein

##residues 80-85, X', 87-99 ##label SHE

GENETICS

#introns 62/3; 81/1; 97/1

#note the first intron occurs in the 5'-untranslated region

CLASSIFICATION #superfamily tumor necrosis factor

KEYWORDS cytokine; cytotoxin; glycoprotein; lymphokine; macrophage;

membrane protein

FEATURE

80-235

. #product tumor necrosis factor #status experimental

86 #binding_site carbohydrate (Asn) (covalent) #status

148-179 #disulfide_bonds #status predicted

SUMMARY #length 235 #molecular_weight 25895 #checksum 8149

Query Match 7.0%; Score 160; DB 1; Length 235;

Best Local Similarity 25.6%; Pred. No. 9.87e-09;

Matches 33; Conservative 34; Mismatches 56; Indels 6; Gaps 6;

Db 107 WLSQRANALLANGMDKDNOLVVPADGLYLVYQVLFKGGCPDYVLLTH-TVSRFAISY 165

QY 186 WYHGRGWAKISN-MTLNGLRVNQDGFYLYANICFRHETSGSVPTDYLQLMVYVVK 244

Db 166 QEKV-NLLSVKSPCKDPPEGAELKPWEPYLVGGVQLEKGDOLAEVNLPKYLDFAE 224

QY 245 SIKIPSSHNLKGGSTKNWNGSEFH-FY-SINVGGFKLAGEEISIQVSNPSLLD-PD 301

Db 225 SGOVYFGVI 233

QY 302 QDATYFGAF 310

RESULT 8

ENTRY A25451 #type complete

TITLE tumor necrosis factor alpha precursor - rabbit

ALTERNATE_NAMES cachectin; TNF alpha

ORGANISM #normal_name Oryctolagus cuniculus #common_name domestic

DATE 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change

ACCESSIONS A25454; A25451; JS0727

REFERENCE A25454

#authors Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara,

J.; Kiyota, T.; Hayashi, H.; Kato, M.; Seko, M.

#journal DNA (1986) 5:149-156

#title Molecular cloning and expression in Escherichia coli of the

cDNA coding for rabbit tumor necrosis factor.

#cross-references MUID:86219711

#accession A25454

##molecule_type mRNA

##residues 1-234 ##label ITO

##cross-references GB:M12845; NID:g165759; PID:g165760

REFERENCE

#authors Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.;

Todd, C.W.; Wallace, R.B.

#journal DNA (1986) 5:157-165

#title Molecular cloning of the gene encoding rabbit tumor necrosis

factor.

#cross-references MUID:86219712

#accession A25451

##molecule_type DNA

##residues 1-234 ##label ITO


```

##note      this sequence differs from that shown in having a Gln
REFERENCE    inserted between residues 62 and 63
#authors     JH0309
#journal      Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.;
#title        Nedospasov, S.A.
#cross-references MUID:91065534
#accession    JS0727
#status       nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues     1-62, 'O', 63-234 ##label SHA
#cross-references GB:M60340; GB:M35326; NID:g165754; PID:g165756
GENETICS     62/3; 80/1; 96/1
#introns      #superfamily tumor necrosis factor
CLASSIFICATION cytokine; cytotoxin; glycoprotein; lymphokine; macrophage;
KEYWORDS      membrane protein
FEATURE       62/3; 80/1; 96/1
1-81          #domain signal sequence #status predicted #label SIG\
82-234        #product tumor necrosis factor #status predicted #label
SUMMARY       #length 234 #molecular-weight 25688 #checksum 664
Query Match   6.6%; Score 152; DB 2; Length 234;
Best Local Similarity 26.0%; Pred. No. 1.52e-07;
Matches 33; Conservative 33; Mismatches 55; Indels 6; Gaps 6;
Db 106 WLSORANALLANGMKLDNOLVVPADGLYLIYSQVLFSGQCRSVLLTH-TVSRFAVS 164
QY 186 WYHGRGWAKISN-MTLNSGKLRVNDGFYLIYANICFRHHTSGVPTDYQLQVMVYVKT 244
Db 165 PNKV-NLLSAIKSPCHTEPEAEPMAYEPIYLGQVFOLEKGRSLSTEVRNOPEVLDLAE 223
QY 245 SIKIPSHNLMKGGSTKNWGNSE-FHY-SINVGGEFKLRAGEISIQVSNPSLLD-PD 301
Db 224 SGQVYFG 230
QY 302 QDATYFG 308
RESULT 9
ENTRY      JU0029
TITLE      tumor necrosis factor alpha precursor - rat
ALTERNATE_NAMES cachectin; TNF alpha
ORGANISM   #formal_name Rattus norvegicus #common_name Norway rat
#sequence_revision 07-Jun-1990 #text_change
ACCESSIONS JU0029; JN0868; S21674
REFERENCE   Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
#authors     Agric. Biol. Chem. (1989) 53:1733-1736
#journal      Cloning and expression in Escherichia coli of the gene for
#title        rat tumor necrosis factor.
#accession    JU0029
#molecule_type DNA
#residues     1-235 ##label SHI
REFERENCE     Kwon, J.; Chung, I.Y.; Benveniste, E.N.
#authors      Gene (1993) 132:227-236
#journal      Cloning and sequence analysis of the rat tumor necrosis
#title        factor-encoding genes.
#accession    JN0868
#molecule_type DNA
#residues     1-235 ##label KWO
#cross-references GB:L00981; NID:g205253; PID:g205254
REFERENCE     Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker,
#authors      K.
#journal      Biol. Chem. Hoppe-Seyler (1992) 373:271-281
#title        Rat tumor necrosis factor-alpha. Transcription in rat Kupffer

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cells and in vitro posttranslational processing based on a
PCR-derived cDNA.
#cross-references MUID:92329007
#accession    S21674
#molecule_type mRNA
#residues     1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 ##label EST
#cross-references GB:X66539; GB:S40199; NID:g395369; PID:g395370
COMMENT       Tumor necrosis factor is secreted by macrophages in response to
endotoxin and produces hemorrhagic necrosis of tumors.
GENETICS     TNF-alpha
#gene         62/3; 81/1; 97/1
CLASSIFICATION #superfamily tumor necrosis factor
KEYWORDS      cytokine; cytotoxin; glycoprotein; lymphokine; macrophage;
membrane protein
FEATURE       #product tumor necrosis factor #status predicted #label
80-235        MAT\
86            #binding_site carbohydrate (Asn) (covalent) #status
SUMMARY       #length 235 #molecular-weight 25806 #checksum 8212
Query Match   6.5%; Score 150; DB 2; Length 235;
Best Local Similarity 25.6%; Pred. No. 3.00e-07;
Matches 33; Conservative 32; Mismatches 58; Indels 6; Gaps 6;
Db 107 WLSORANALLANGMKLDNQLVVPADGLYLIYSQVLFQGGCPDYVLLTH-TVSRFAIS 165
QY 186 WYHGRGWAKISN-MTLNSGKLRVNDGFYLIYANICFRHHTSGVPTDYQLQVMVYVKT 244
Db 166 QKV-SILSAIKSPCKPTPEGAELKPWEPYLVGVFOLEKGLLSAEVNLPKYLDITE 224
QY 245 SIKIPSHNLMKGGSTKNWGNSEFH-FY-SINVGGEFKLRAGEISIQVSNPSLLD-PD 301
Db 225 SGQVYFGVI 233
QY 302 QDATYFGAF 310
RESULT 10
ENTRY      S21738
TITLE      #type complete
ORGANISM    CD40 ligand - mouse
#formal_name Mus musculus #common_name house mouse
#sequence_revision 31-Dec-1993 #text_change
ACCESSIONS S21738
REFERENCE   Armistage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.;
#authors     Clifford, K.N.; Macduff, B.M.; Anderson, D.M.; Gimpel,
S.D.; Davis-Smith, T.; Maliszewski, C.R.; Clark, E.A.;
Smith, C.A.; Grabstein, K.H.; Cosman, D.; Spriggs, M.K.
#journal      Nature (1992) 357:80-82
#title        Molecular and biological characterization of a murine ligand
for CD40.
#cross-references MUID:92244364
#accession    S21738
#molecule_type mRNA
#residues     1-260 ##label ARM
#cross-references EMBL:X65453; NID:g50351; PID:g50352
KEYWORDS      glycoprotein; transmembrane protein
FEATURE       23-46
47-260        #domain transmembrane #status predicted #label TMM\
239            #domain extracellular #status predicted #label EXT\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY       #length 260 #molecular-weight 29396 #checksum 9490
Query Match   6.5%; Score 150; DB 2; Length 260;
Best Local Similarity 29.6%; Pred. No. 3.00e-07;
Matches 48; Conservative 49; Mismatches 47; Indels 18; Gaps 16;
Db 113 ORGDEDPQIAAHV-VSEAN-SNAA-SV-LQ-W-AKGGYTMKSNLVMLENGKOLTVKREG 166
||| ::| ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|

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Qy	155	GRGPEAQPFAHLTTNAASIPSGSHUKVTLSSSHWDGHW-AKISNMT-LSNGK-LRVNQDG	211	
Db	167	LYYVYQTVTFCSNRFPSSORP--FI-VGLWL-KPSI--GSERILLKAANTHSSSQLCE-Q	219	
Qy	212	FYYLYANICF-RHHTSGSVPTDYQLQLMVYVVKTSIKIPSSHNLMKGGSTKNWGNSEFH	270	
Db	220	-OSVHLGGVFELQAGASVFNVTAEASQVTHRVFGFSFGLLKL	260	
Qy	271	FYSINVGGFFKLKRAEEISIQVSNPSLLDPDQDATYFGAFV	312	
RESULT	11			
ENTRY		154490	#type complete	
TITLE		tumor necrosis factor - white-footed mouse		
ORGANISM		#formal_name Peromyscus leucopus	#common_name white-footed mouse	
DATE		02-Aug-1996	#sequence_revision 02-Aug-1996	#text_change 23-Feb-1997
ACCESSIONS		154490		
REFERENCE		154490		
#authors		Crew, M.D.; Filipowsky, M.E.		
#journal		Immunogenetics (1992) 35:351-353		
#title		Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus (family Cricetidae).		
#cross-references		MUID:92218012		
#accession		154490		
#status		preliminary; translated from GB/EMBL/DBDJ		
#molecule_type		DNA		
#residues		1-235	#label RES	
#cross-references		GB:M59233; NID:g202506; PID:g202507		
GENETICS				
#gene		PLTNF		
#introns		62/3; 81/1; 97/1		
CLASSIFICATION		#superfamily tumor necrosis factor		
SUMMARY		#length 235	#molecular-weight 25822	#checksum 8367
Query Match		6.3%;	Score 145;	DB 2; Length 235;
Best Local Similarity		26.3%;	Prev. No. 1.60e-06;	
Matches		31; Conservative	29; Mismatches 53;	Indels 5; Gaps 5;
Db	118	NGMDLKDNLQVLPADGLILVYQVLFKGGCCSSVLLTH-TVSRFAVSVDKY-NLLSAI	175	
Qy	196	SNMTLSNGKLRVYNQDGFYLYANICFRHHTSGSVPTDYQLQLMVYVVKTSIKIPSSHNLM	255	
Db	176	KSPCKPTEPGSELPTWPEIYLVGVFQLEKGRLSAEVNLPKYLDFAESGQYVFGVI	233	
Qy	256	KGGSTKNWGNSEFH-FY-SINVGGFFKLKRAEEISIQVSNPSLLD-PDQDATYFGAF	310	
RESULT	12			
ENTRY		JQ1344	#type complete	
TITLE		tumor necrosis factor alpha precursor - horse		
ALTERNATE_NAMES		cachectin; TNF alpha		
ORGANISM		#formal_name Equus caballus	#common_name domestic horse	
DATE		30-Jun-1992	#sequence_revision 30-Jun-1992	#text_change 08-Sep-1997
ACCESSIONS		JQ1344		
REFERENCE		JQ1344		
#authors		Su, X.; Morris, D.D.; McGraw, R.A.		
#journal		Gene (1991) 107:319-321		
#title		Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor alpha.		
#cross-references		MUID:92084125		
#accession		JQ1344		
#molecule_type		DNA		
#residues		1-234	#label SUX	
#cross-references		GB:M64087; NID:g164244; PID:g164245		
COMMENT		This protein is an important proximal mediator of endotoxemia.		
GENETICS				
#gene		TNF-alpha		
#introns		62/3; 79/1; 95/1		
CLASSIFICATION		#superfamily tumor necrosis factor		
KEYWORDS		cytokine; cytotoxin; glycoprotein; lymphokine; macrophage;		

QY	224	HETSGSVPTDYQLQMLVYVVKYSIKIPSSHNLMKGGSTKNWGSNSPEHFYSINVGGEFKLR	283
Db	118	AGASVFNVTPEASQVHRVGFSSFGLLKL	146
QY	284	AGEISIQVSNPSLLDPDQDATYFGAFKV	312
RESULT	14		
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W P S R L H (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Fri Nov 13 17:19:15 1998; MasPar time 3.46 Seconds
647.079 Million cell updates/sec
ular output not generated.

Title: >US-08-989-362-2
Description: (1-316) from US08989362.pep
Perfect Score: 2294
Sequence: 1 MRRASRDYCKYLRSSEMGs.....LLDPQDQATYFGAFKVVOD1 316

Scoring table: PAM 150
Gap 11

Searched: 77309 seqs, 7078906 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 31.764; Variance 144.069; scale 0.220

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	326	14.2	281	1	US-08-670- Sequence 2, Applicatio	9.86e-19
2	326	14.2	281	2	PCT-US96-1 Sequence 2, Applicatio	9.86e-19
3	282	12.3	291	1	US-08-670- Sequence 6, Applicatio	6.84e-15
4	282	12.3	291	2	PCT-US96-1 Sequence 6, Applicatio	6.84e-15
5	175	7.6	279	2	PCT-US95-0 Sequence 2, Applicatio	7.32e-06
6	170	7.4	279	2	PCT-US95-0 Sequence 5, Applicatio	1.86e-05
7	167	7.3	151	1	US-07-940- Sequence 3, Applicatio	3.25e-05
8	165	7.2	261	1	US-08-360- Sequence 2, Applicatio	4.71e-05
9	165	7.2	261	1	US-08-446- Sequence 4, Applicatio	4.71e-05
10	165	7.2	261	1	US-07-940- Sequence 2, Applicatio	4.71e-05
11	165	7.2	261	1	US-08-184- Sequence 8, Applicatio	4.71e-05
12	165	7.2	261	2	PCT-US93-1 Sequence 4, Applicatio	4.71e-05
13	165	7.2	273	1	US-08-446- Sequence 11, Applicati	4.71e-05
14	162	7.1	157	2	PCT-US93-0 Sequence 9, Applicatio	8.20e-05
15	154	6.7	151	1	US-07-940- Sequence 4, Applicatio	3.57e-04
16	148	6.5	157	2	PCT-US93-0 Sequence 7, Applicatio	1.06e-03
17	148	6.5	157	2	PCT-US93-0 Sequence 8, Applicatio	1.06e-03
18	142	6.2	260	2	US-08-446- Sequence 6, Applicatio	3.14e-03
19	142	6.2	260	2	PCT-US93-1 Sequence 6, Applicatio	3.14e-03
20	141	6.1	158	1	US-07-794- Sequence 6, Applicatio	3.76e-03
21	141	6.1	158	1	US-08-397- Sequence 6, Applicatio	3.76e-03
22	136	5.9	150	1	US-07-668- Sequence 12, Applicati	9.19e-03
23	136	5.9	151	1	US-07-668- Sequence 26, Applicati	9.19e-03

24	136	5.9	155	1	US-07-994- Sequence 94, Applicati	9.19e-03
25	135	5.9	157	2	PCT-US93-0 Sequence 4, Applicatio	9.19e-03
26	136	5.9	158	1	US-07-994- Sequence 99, Applicatio	9.19e-03
27	135	5.9	158	1	US-08-397- Sequence 7, Applicatio	1.10e-02
28	135	5.9	158	1	US-07-794- Sequence 7, Applicatio	1.10e-02
29	134	5.8	155	1	US-07-994- Sequence 76, Applicati	1.31e-02
30	133	5.8	155	1	US-07-994- Sequence 3, Applicatio	1.31e-02
31	134	5.8	158	1	US-07-994- Sequence 82, Applicati	1.31e-02
32	133	5.8	158	1	US-08-397- Sequence 8, Applicatio	1.57e-02
33	133	5.8	158	1	US-07-794- Sequence 8, Applicatio	1.57e-02
34	130	5.7	154	1	US-07-994- Sequence 75, Applicati	2.66e-02
35	131	5.7	155	1	US-07-994- Sequence 92, Applicati	2.66e-02
36	130	5.7	155	1	US-07-994- Sequence 13, Applicati	2.66e-02
37	130	5.7	155	1	US-07-994- Sequence 5, Applicatio	2.66e-02
38	130	5.7	157	1	US-07-994- Sequence 81, Applicati	2.66e-02
39	130	5.7	157	1	US-07-940- Sequence 5, Applicatio	2.66e-02
40	131	5.7	158	1	US-07-994- Sequence 97, Applicati	2.23e-02
41	129	5.6	139	1	US-07-994- Sequence 10, Applicati	3.17e-02
42	129	5.6	145	1	US-07-994- Sequence 9, Applicatio	3.17e-02
43	129	5.6	155	1	US-07-994- Sequence 93, Applicati	3.17e-02
44	129	5.6	155	1	US-07-994- Sequence 79, Applicati	3.17e-02
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ALIGNMENTS

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ID	US-08-670-354-2			
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DE	Sequence 2, Application US/08670354			
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CC	Sequence 2, Application US/08670354			
CC	Patent No. 5763223			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Steven R. Wiley and			
CC	APPLICANT: Raymond G. Goodwin.			
CC	TITLE OF INVENTION: Cytokine That Induces Apoptosis			
CC	NUMBER OF SEQUENCES: 9			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: Kathryn A. Anderson, Immunex Corporation			
CC	STREET: 51 University Street			
CC	CITY: Seattle			
CC	STATE: WA			
CC	COUNTRY: USA			
CC	ZIP: 98101			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: Apple Macintosh			
CC	OPERATING SYSTEM: Apple 7.5.2			
CC	SOFTWARE: Microsoft Word, Version 6.0.1			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/670.354			
CC	FILING DATE: 25-JUN-1996			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: US 08/496.632			
CC	FILING DATE: 29-JUN-1995			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: US 08/548.368			
CC	FILING DATE: 01-NOV-1995			
CC	CLASSIFICATION: 435			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Anderson, Kathryn A.			
CC	REGISTRATION NUMBER: 32,172			
CC	REFERENCE/DOCKET NUMBER: 2835-B			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: (206) 587-0430			
CC	TELEFAX: (206) 233-0644			

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 291 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 291 AA; 33477 MW; 453904 CN;
Query Match 12.3%; Score 282; DB 1; Length 291;
Best Local Similarity 35.8%; Pred. No. 6.84e-15;
Matches 48; Conservative 37; Mismatches 42; Indels 8; Gaps 5;
Db 155 IESWESSRKGSHFLNHLFRNGELVIEQGLYIYISQTYFRFOEAEDASKMVKDKVTK 214
QY 183 LSSWYHDR-GWAKISNMTLSNGLRVNQDGFYLYANICFRHET-SGS--VPTDYL--- 235
Db 215 QLVQYIYKYT-SYPDPVILMKSNRSDAEYGLYSIQGGLFELKKNDRIFVSVTNE 273
QY 236 QLMVYVVKTSIKIPSSHNLKMGSGTKNSGSEFHFYSINVGFFKLAGEEISIQVSNP 295
274 HLMDDOEASFEGAF 288
296 SLDDPDQDATYFGAF 310

RESULT 4
ID PCT-US96-10895-6 STANDARD; PRT; 291 AA.
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AC xxxxxx
XX
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XX
DE Sequence 6, Application PC/TUS9610895
XX Sequence 6, Application PC/TUS9610895
CC GENERAL INFORMATION:
CC APPLICANT: Immunex Corporation.
CC TITLE OF INVENTION: Cytokine That Induces Apoptosis
CC NUMBER OF SEQUENCES: 9
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.5.2
CC SOFTWARE: Microsoft Word, Version 6.0.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US96/10895
CC FILING DATE: 25-JUN-1996
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/496,632
CC FILING DATE: 29-JUN-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/548,368
CC FILING DATE: 01-NOV-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Anderson, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2835-WO
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 587-0430
CC TELEFAX: (206) 233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 291 amino acids

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 291 AA; 33477 MW; 453904 CN;
Query Match 12.3%; Score 282; DB 2; Length 291;
Best Local Similarity 35.6%; Pred. No. 6.84e-15;
Matches 48; Conservative 37; Mismatches 42; Indels 8; Gaps 5;
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QY 183 LSSWYHDR-GWAKISNMTLSNGLRVNQDGFYLYANICFRHET-SGS--VPTDYL--- 235
Db 215 QLVQYIYKYT-SYPDPVILMKSNRSDAEYGLYSIQGGLFELKKNDRIFVSVTNE 273
QY 236 QLMVYVVKTSIKIPSSHNLKMGSGTKNSGSEFHFYSINVGFFKLAGEEISIQVSNP 295
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296 SLDDPDQDATYFGAF 310
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DE Sequence 2, Application PC/TUS9500362
XX Sequence 2, Application PC/TUS9500362
CC GENERAL INFORMATION:
CC APPLICANT: IMMUNEX CORPORATION
CC TITLE OF INVENTION: Ligand That Binds Fas Antigen
CC NUMBER OF SEQUENCES: 5
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: US
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/00362
CC FILING DATE: 06-JAN-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/179,138
CC FILING DATE: 07-JAN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/190,559
CC FILING DATE: 01-FEB-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Anderson, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2805-WO
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 281 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 281 AA; 31485 MW; 464188 CN;
Query Match 7.6%; Score 175; DB 2; Length 281;
Best Local Similarity 23.9%; Pred. No. 7.32e-06;
Matches 44; Conservative 55; Mismatches 75; Indels 10; Gaps 8;

xxxxxx

Sequence 2, Application US/07940605A

Sequence 2, Application US/07940605A

Patent No. 5540926

GENERAL INFORMATION:

APPLICANT: ARUFFO, ALEJANDRO

APPLICANT: HOLLEBAUGH, DIANE

APPLICANT: LEDBETTER, JEFFREY A.

TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/940.605A

FILING DATE: 04-SEP-1992

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 5624-184

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 261 AA; 29273 MW; 363115 CN;

Query Match 7.2%; Score 165; DB 1; Length 261;

Best Local Similarity 29.5%; Pred. No. 4.71e-05;

Matches 44; Conservative 47; Mismatches 44; Indels 14; Gaps 12;

Db 122 IAAHVISEASSKTTSVLOW-AEKGYTMSNNLVTLENGKQLTVKROGLYIYAQVTFCSN 180

Qy 169 INAAISPGSHKVT-LSSWYHDSRGWAKISN-M-TLSNGK-LRVNODGFYLYANICF-RH 223

Db 181 REASSQAP--FTASL-CL-KSPGRF--ERILLRAANTHS-SAKPCGO-QSIHLGGVFEIQ 232

Qy 224 HETSSVPTDYQLVMVYVVKTSIKIPSSHNLMKGGSTKNWSEHFYSINVGFFKLK 283

Db 233 PGASVFNVTDPQSQVSHGTGFTSFGLLKL 261

Qy 284 AGEETSIQVSNPSLLDPDQDATYFGAFKV 312

RESULT 11

ID US-08-184-422-8 STANDARD; PRT; 261 AA.

XX xxxxxx

Sequence 6, Application US/08184422

Sequence 8, Application US/08184422

Patent No. 5565321

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: DAVISON, BARRY

APPLICANT: FANSHAW, WILLIAM

APPLICANT: RENSCHAW, BLAIR

APPLICANT: SPRIGGS, MELANIE

APPLICANT: WIDMER, MICHAEL

TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS

TITLE OF INVENTION: IN A CD40 LIGAND GENE

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple Operating System 7.1

SOFTWARE: MS Word for Apple 5.1, Version a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/184.422

FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/009,258

FILING DATE: 01/22/93

ATTORNEY/AGENT INFORMATION:

NAME: PERKINS, PATRICIA ANNE

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2810-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430

TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 261 AA; 29273 MW; 363115 CN;

Query Match 7.2%; Score 165; DB 1; Length 261;

Best Local Similarity 29.5%; Pred. No. 4.71e-05;

Matches 44; Conservative 47; Mismatches 44; Indels 14; Gaps 12;

Db 122 IAAHVISEASSKTTSVLOW-AEKGYTMSNNLVTLENGKQLTVKROGLYIYAQVTFCSN 180

Qy 169 INAAISPGSHKVT-LSSWYHDSRGWAKISN-M-TLSNGK-LRVNODGFYLYANICF-RH 223

Db 181 REASSQAP--FTASL-CL-KSPGRF--ERILLRAANTHS-SAKPCGO-QSIHLGGVFEIQ 232

Qy 224 HETSSVPTDYQLVMVYVVKTSIKIPSSHNLMKGGSTKNWSEHFYSINVGFFKLK 283

Db 233 PGASVFNVTDPQSQVSHGTGFTSFGLLKL 261

Qy 284 AGEETSIQVSNPSLLDPDQDATYFGAFKV 312

RESULT 12

ID PCT-US93-10034-4 STANDARD; PRT; 261 AA.

XX xxxxxx

Sequence 4, Application PC/TUS9310034

Sequence 4, Application PC/TUS9310034

[illegible]

CC	STREET: 51 University Street
CC	CITY: Seattle
CC	STATE: WA
CC	COUNTRY: USA
CC	ZIP: 98101
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: Apple Macintosh
CC	OPERATING SYSTEM: Apple Operating System 7.1
CC	SOFTWARE: Microsoft Word for Apple, Version 5.1a
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/446,922
CC	FILING DATE:
CC	CLASSIFICATION: 435
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: USSN 08/107,353
CC	FILING DATE: 08-13-93
CC	CLASSIFICATION: 435
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Perkins, Patricia A
CC	REGISTRATION NUMBER: 34,693
CC	REFERENCE/DOCKET NUMBER: 1003-A
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: (206)587-0430
CC	TELEFAX: (206)233-0644
CC	INFORMATION FOR SEQ ID NO: 11:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 273 amino acids
CC	TYPE: amino acid
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein
CC	SEQUENCE 273 AA; 30821 MW; 395120 CN;
Query Match	7.2%; Score 165; DB 1; Length 273;
Best/Local Similarity	29.5%; Pred.No. 4.7le-05;
Matches 44; Conservative 47; Mismatches 44; Indels 14; Gaps 14	
Db	134 IAAHVISEASKKTTSVLQW-AERGYTMSNNLVLENGKQLTVKRGLYIYAQVTFCSN 192
Qy	169 INAAISPGSHKVT-LSSWYHDSRWAKISN-W-TLSNGK-LRVNODGFYLYANICF-RH 223
Db	193 REASSQAP--FIASL-CL-KSPGRF--ERILLRAANTHS-SAKPCGQ-QSIHLGGVFELQ 244
Qy	224 HETSGSVPTDYLQVMYVYVKTISKIPSSHLMKMGSTKNWGNSEPHFYISNVGGFFKL 283
Db	245 PGASVFVNVTDPSQVSHGTFSTFGLKL 273
Qy	284 AGEISIQVSNPSLLDPDQDATYFGAKV 312
RESULT 14	
ID	PCT-US93-02475-9 STANDARD; PRT; 157 AA.
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DT	
XX	
DE	Sequence 9, Application PC/TUS9302475
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CC	Sequence 9, Application PC/TUS9302475
CC	GENERAL INFORMATION:
CC	APPLICANT: Wisnieski, Bernadine J.
CC	TITLE OF INVENTION: Tumor Necrosis Factor with Modified
CC	TITLE OF INVENTION: Ion Channel
CC	NUMBER OF SEQUENCES: 13
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Donald G. Lewis
CC	STREET: 8328 Regents Road #1E
CC	CITY: San Diego
CC	STATE: California
CC	COUNTRY: USA
CC	ZIP: 92122
CC	COMPUTER READABLE FORM:

CC		STREET:	51 University Street
CC		CITY:	Seattle
CC		STATE:	WA
CC		COUNTRY:	USA
CC		ZIP:	98101
CC		COMPUTER READABLE FORM:	
CC		MEDIUM TYPE:	Floppy disk
CC		COMPUTER:	Apple Macintosh
CC		OPERATING SYSTEM:	Apple Operating System 7.1
CC		SOFTWARE:	Microsoft Word for Apple, Version 5.1a
CC		CURRENT APPLICATION DATA:	
CC		APPLICATION NUMBER:	US/08/446,922
CC		FILING DATE:	
CC		CLASSIFICATION:	435
CC		PRIOR APPLICATION DATA:	
CC		APPLICATION NUMBER:	USSN 08/107,353
CC		FILING DATE:	08-13-93
CC		CLASSIFICATION:	435
CC		ATTORNEY/AGENT INFORMATION:	
CC		NAME:	Perkins, Patricia A.
CC		REGISTRATION NUMBER:	34,693
CC		REFERENCE/DOCKET NUMBER:	1003-A
CC		TELECOMMUNICATION INFORMATION:	
CC		TELEPHONE:	(206)587-0430
CC		TELEFAX:	(206)233-0644
CC		INFORMATION FOR SEQ ID NO:	11:
CC		SEQUENCE CHARACTERISTICS:	
CC		LENGTH:	273 amino acids
CC		TYPE:	amino acid
CC		TOPOLOGY:	linear
CC		MOLECULE TYPE:	protein
CC		SEQUENCE	273 AA; 30821 MW; 395120 CN;
SQ			
		Query Match	7.28; Score 165; DB 1; Length 273;
		Best Local Similarity	29.58; Pred.No.4.7le-05;
		Matches	44; Conservative 47; Mismatches 44; Indels 14
Dd		134	IAAHVISEASKTSVTSLVW--AERGYYTMMNNLTLENGKOLTVVKROGLYIYAQQV : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy		169	INAASIPSGSHKYT-LSSWDHGRGWAKISN-M-TLSNGK-LRVNQDGFYLXANI : : : : : : : : : : : : : : : :
Dd		193	REASSQAP--FIASL-CL-KSPGRF--ERILLRAANTHS-SAKPCGO-QSIHLGGG : : : : : : : : : : : : : : : : :
Qy		224	HETSGSVYTDLYLMVVVYVTKISKPSSHNLMKGGSTKNWSGNSEFHYSINVGVG : : : : : : : : : : : : : : : : :
Dd		245	PGASVFVNVDPSOVSHGTGTFSGLLKL 273 : : : : : : : : : : : : : : : : :
Qy		284	AGEEISIQVSNPSSLDDPDQDATYGAFKV 312 : : : : : : : : : : : : : : : : :
RESULT		14	
ID		PCT-US93-02475-9	STANDARD; PRI; 157 AA..
XX		xxxxxxx	
AC			
XX			
DT			
XX			
DE		Sequence 9, Application PC/TUS9302475	
XX			
CC		Sequence 9, Application PC/TUS9302475	
CC		GENERAL INFORMATION:	
CC		APPLICANT:	Wisnleski, Bernadine J.
CC		TITLE OF INVENTION:	Tumor Necrosis Factor with Modified
CC		TITLE OF INVENTION:	Ion Channel
CC		NUMBER OF SEQUENCES:	13
CC		CORRESPONDENCE ADDRESS:	
CC		ADDRESSEE:	Donald G. Lewis
CC		STREET:	8328 Regents Road #1E
CC		CITY:	San Diego
CC		STATE:	California
CC		COUNTRY:	USA
CC		ZIP:	92122
CC		COMPUTER READABLE FORM:	

CC MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage
 CC COMPUTER: VE System 386
 CC OPERATING SYSTEM: MS-DOS 5
 CC SOFTWARE: Word Perfect
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/02475
 CC FILING DATE: 19930412
 CC CLASSIFICATION:

PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/852,625
 CC FILING DATE: 12 March 1992
 CC ATTORNEY/AGENT INFORMATION:

CC NAME: Donald G. Lewis

CC REGISTRATION NUMBER: 28636

CC REFERENCE/DOCKET NUMBER: BJW-2

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (619) 554-2421

CC TELEFAX: (619) 554-6312

CC INFORMATION FOR SEQ ID NO: 9:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 157 amino acids

CC TYPE: AMINO ACIDS

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC FEATURE:

CC NAME/KEY: Tumor Necrosis Factor (murine)

CC OTHER INFORMATION: A blank residue designated by

CC OTHER INFORMATION: "Xaa" is inserted after residue No. 70 of murine

CC OTHER INFORMATION: TNF and the sequence numbering is augmented by 1

CC OTHER INFORMATION: starting with residue No. 71 in order to maximize

CC OTHER INFORMATION: the sequence homology with human TNF.

CC PUBLICATION INFORMATION:

CC AUTHORS: Caput, D., Beutler, B. Hartog, K.

CC AUTHORS: Thayer, R., Brown-Shimer, S. and

CC AUTHORS: Cerami, A.

CC TITLE: Identification of a Common Nucleotide

CC TITLE: Sequence in the 3'-Untranslated Region of mRNA

CC TITLE: Molecules Specifying Inflammatory Mediators.

CC JOURNAL: Proc. National Academy of Science,

CC JOURNAL: U.S.A.

CC VOLUME: 83

CC PAGES: 1670-1674

CC DATE: 1986

CC RELEVANT RESIDUES IN SEQ ID NO: 9: 1-157 (includes

CC RELEVANT RESIDUES IN SEQ ID NO: one blank)

CC SEQUENCE 157 AA; 17304 MW; 137297 CN;

Query Match 7.1%; Score 162; DB 2; Length 157;

Best Local Similarity 25.6%; Pred. No. 8.20e-05;

Matches 33; Conservative 34; Mismatches 57; Indels 5; Gaps 5;

Db 28 WLSQRANALLANGMDLKDNLVVPADGLVLYVSOVLFGQGPXDVLTHVTSRFAISY 87

QY 186 WYHWRGAKISN-MTSLNGKLVRNODGFFLYLANICFRHETSGSVPTDYQLQMLVYVVK 244

Db 88 QEKV-NLLSAVKSPCKDPPEGAELKPWEPIYLGQVFOLEKQDLSAEVNLPKYLDFAE 146

QY 245 SKIPSSHNLKMGSTKNWNSGEFH-FY-SINVGFFKLRAGEEISIQVNSPLLD-PD 301

Db 147 SGQVYFGVI 155

QY 302 QDATYFGAF 310

RESULT 15

XX US-07-940-605A-4 STANDARD; PRT; 151 AA.

AC xxxxxx

XX

DT

XX

DE

XX

Sequence 4, Application US/07940605A

CC Sequence 4, Application US/07940605A
 CC Patent No. 5540926
 CC GENERAL INFORMATION:
 CC APPLICANT: ARUFFO, ALEJANDRO
 CC APPLICANT: HOLLENBAUGH, DIANE
 CC APPLICANT: LEDBETTER, JEFFREY A.
 CC TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
 CC NUMBER OF SEQUENCES: 15
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Pennie & Edmonds
 CC STREET: 1155 Avenue of the Americas
 CC CITY: New York
 CC STATE: New York
 CC COUNTRY: U.S.A.
 CC ZIP: 10036-2711
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/940,605A
 CC FILING DATE: 04-SEP-1992
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Misrock, S. Leslie
 CC REGISTRATION NUMBER: 18,872
 CC REFERENCE/DOCKET NUMBER: 5624-184
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 212 790-9090
 CC TELEFAX: 212 869-8864/9741
 CC TELEX: 66141 PENNIE
 CC INFORMATION FOR SEQ ID NO: 4:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 151 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 151 AA; 16904 MW; 127489 CN;

Query Match 6.7%; Score 154; DB 1; Length 151;

Best Local Similarity 30.8%; Pred. No. 3.57e-04;

Matches 45; Conservative 45; Mismatches 38; Indels 18; Gaps 16;

Db 4 ORQDEDPQIAAHV-VSEAN-SNAA-SV-LQ-W-AKGGYTKSNLYMLENGKQLTVKREG 57

QY 155 ORQKPEAQPFALHTINAASIPSGSHKVTLSSTWYHDRGW-AKISNMT-LSNGK-LRVNODG 211

Db 58 LYYVYQVTFCSNREPSSORP--FI-VGLWL-KPSI--GSEKILLKAANTHSSSOLCE-Q 110

QY 212 FYLYANICF-RHETSGSVPTDYQLQMLVYVVKTSIKIPSSHNLKMGSTKNWNSGEFH 270

Db 111 -OSVHLGGYFELQAGASVFVNVTAS 135

QY 271 FYSINVGFFKLRAGEEISIQVSNPS 296

Search completed: Fri Nov 13 17:19:44 1998

Job time : 29 secs.

DQ 211 YKVT-SYPDIPILLKMSARNSCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMD 269
 QY 242 VTKSIKIPSSHNLKMGSTKNWNGSEFHYFYSINVGFFKLRAGEEISIQVSNPSLLDPD 301

Db 270 HEASPFAGFLV 280
 QY 302 QDATYFGAFKV 312

RESULT 2
 ID TRAIL MOUSE STANDARD; PRT; 291 AA.
 AC P50592;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE TNF-RELATED APOPTOSIS INDUCING LIGAND (TRAIL PROTEIN).
 GN TRAIL.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 96111955.
 RA WILEY S.R., SCHOOLEY K., SMOLAK P.J., DIN W.S., HUANG C.-P.,
 RA NICHOLL J.K., SUTHERLAND G.R., DAVIS-SMITH T., RAUCH C., SMITH C.A.,
 RA GOODWIN R.G.;
 RL IMMUNITY 3:673-682(1995).

CC -1- FUNCTION: INDUCES APOPTOSIS.
 CC -1- SUBUNIT: HOMOTRIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 DR EMBL: U37522; G1149560;
 DR MGD; MGI:107414; TRAIL.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 KW CYTOKINE; TRANSMEMBRANE; SIGNAL-ANCHOR; APOPTOSIS.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 52 52 POTENTIAL.
 SQ SEQUENCE 291 AA; 33477 MW; F9906FBE CRC32;

Query Match 12.3%; Score 282; DB 1; Length 291;
 Best Local Similarity 35.6%; Pred. No. 7.11e-35;
 Matches 48; Conservative 37; Mismatches 42; Indels 8; Gaps 5;

DQ 155 IESWESSRKGHSLNHLVFRNGELVIEQGLYIYQTYFRQEAEDASKWVSKDKVRTK 214
 QY 183 LSSWYHNR-GWAKISNMTLSNGLRYNQDGFYLYXANICFRHET-SGS--VPTDYL--- 235

Db 215 QLVQYIYKVT-SYDPDVLKMSARNSCKSDAEYGLYSIYQGGIFELKNDRIFFSVTNE 273
 QY 236 QLMVYVVKTSIKIPSSHNLKMGSTKNWNGSEFHYFYSINVGFFKLRAGEEISIQVSNP 295

Db 274 HLMDLQEAFFGAF 288
 QY 296 SLDDPDQDATYFGAF 310

RESULT 3
 ID FASL RAT STANDARD; PRT; 278 AA.
 AC P36940;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE FAS ANTIGEN LIGAND.
 GN APTLIG1 OR FASL.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 94084792.
 RA SUDA T., TAKAHASHI T., GOLSTEIN P., NAGATA S.;
 RL CELL 75:1169-1178(1993).
 CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN. A RECEPTOR THAT
 CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
 CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
 CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
 CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
 CC T CELLS, OR BOTH.
 CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
 CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
 CC SURFACE.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
 CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
 CC KIDNEY AND LUNG.
 CC -1- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

DR EMBL: U03470; G440179;
 DR HSSP; P19999; ICLG.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 KW CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR; APOPTOSIS.
 FT DOMAIN 1 77 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 78 99 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 100 278 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 4 69 PRO-RICH.
 FT DOMAIN 45 58 POLY-PRO.
 FT DISULFID 199 230 BY SIMILARITY.
 FT CARBOHYD 116 116 POTENTIAL.
 FT CARBOHYD 247 247 POTENTIAL.
 FT CARBOHYD 257 257 POTENTIAL.
 FT CARBOHYD 116 116 POTENTIAL.
 FT CARBOHYD 247 247 POTENTIAL.
 FT CARBOHYD 257 257 POTENTIAL.
 SQ SEQUENCE 278 AA; 31140 MW; 6DC17725 CRC32;

Query Match 7.6%; Score 174; DB 1; Length 278;
 Best Local Similarity 26.7%; Pred. No. 1.89e-13;
 Matches 36; Conservative 38; Mismatches 53; Indels 8; Gaps 6;

Db 152 SRSIPLE-WEDTYGTALISGVKYGKGLVINEAGLYFVYSKVYFRGQ-SCNSQP---LSH 206
 QY 178 SHKVLSSWYHNRGWAKISNMTLSNGLRYNQDGFYLYXANICFRHETSGSVPTDYLQL 237

Db 207 KVMY-R-NFYPGDLVLMEE-KKLNYCTTGQIWAHSSYLGAVNLTVAHDHLYVNIQSLSL 263
 QY 238 MVYVVKTSIKIPSSHNLKMGSTKNWNGSEFHYFYSINVGFFKLRAGEEISIQVSNPSL 297

Db 264 INFEEKTFYGLYKL 278
 QY 298 LDPPDQDATYFGAFKV 312

RESULT 4
 ID FASL HUMAN STANDARD; PRT; 281 AA.
 AC F48023;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
 GN APTLIG1 OR FASL.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95105731.
 RA ALDERSON M.;
 RL J. EXP. MED. 181:71-77(1995).
 RN [2]
 RP SEQUENCE FROM N.A.

[illegible]

QY 178 SHKVTLSWYHGRGWAKISNMTLSNGKLRVQDGFYLYANICFRHHTSGSVPTDYLQL 237
Db 208 KYVM-RNS-KYPEDVLMEERKL-NYCTGQIWAHSSVLGAVFNLTSDHLYVNISQLSL 264
QY 238 MIVVVKTSIKIPSSHLMKGGSTKNWNSGFHFSYINVGFFKLRLAGEEISIQVNP 297
Db 265 INFESCTFFGLYKL 279
QY 298 LDPQDATYFGAFKV 312
RESULT 6
ID CD4L HUMAN STANDARD; PRT; 261 AA.
AC P29955;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE CD40 LIGAND (CD40-L) (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL
DE ANTIGEN GP39) (CD154 ANTIGEN).
CN CD40LG OR CD40L OR TRAP.
OC HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; PRIMATES.
[1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 93076854.
RA GRAF D., KORTHAUER U., MAGES H.W., SENGGER G., KROCZEK R.A.;
RL EUR. J. IMMUNOL. 22:3191-3194(1992).
[2]
RX SEQUENCE FROM N.A.
RX MEDLINE; 93049181.
RA HOLLENBAUGH D., GROSMAIRE L., KULLAS C., CHALUPNY J.,
RA BRAESCH-ANDERSEN S., NOELLE R., STAMENKOVIC I., LEDBETTER J.,
RA ARUFFO A.;
RL EMBO J. 11:4313-4321(1992).
[3]
RX SEQUENCE FROM N.A.
RX MEDLINE; 93145330.
RA SPRIGGS M.K., ARMITAGE R.J., STOCKBINE L., CLIFFORD K.N.,
RA MACDUFF B.M., SATO T.A., MALISZEWSKI C.R., FANSLW W.C.;
RL CELL 72:291-300(1993).
[4]
RX SEQUENCE FROM N.A.
RX MEDLINE; 93094757.
RA SPRIGGS M.K., ARMITAGE R.J., STOCKBINE L., CLIFFORD K.N.,
RA MACDUFF B.M., SATO T.A., MALISZEWSKI C.R., FANSLW W.C.;
RL J. EXP. MED. 176:1543-1550(1992).
[5]
RX SEQUENCE FROM N.A.
RX MEDLINE; 93138085.
RA GAUCHAT J.F.M., AUBRY J., MAZZEI G.J., LIFE P., JOMOTTE T., ELSON G.,
RA BORNEFOY J.Y.;
RL FEBS LETT. 315:259-266(1993).
[6]
RX SEQUENCE FROM N.A.
RA SHIMADZU M., TERASAKI H., NINOMIYA R., SHIMIZU S., NUNOI H.,
RA MATSUDA I.;
RL SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
[7]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261.
RX MEDLINE; 96131874.
RA KARPSUSAS M., HSU Y.-M., WANG J.-H., THOMPSON J., LEDERMAN S.,
RA CHESSE L., THOMAS D.;
RL STRUCTURE 3:1031-1039(1995).
[8]
RX VARIANTS HIGM1 ARG-36 AND GLY-140.
RX MEDLINE; 93156839.
RA KORTHAUER U., GRAF D., MAGES H.W., BRIERE F., PADAYACHEE M.,
RA MALCOLM S., UGAZIO A.G., NOTARANGELO L.D., LEVINSKY R.J.,
RA KROCZEK R.A.;
RL NATURE 361:539-541(1993).
[9]
RX VARIANT HIGM1 GLU-123.
KW

RX MEDLINE; 93156840.
RA DISANTO J.P., BONNEFOY J.Y., GAUCHAT J.F., FISCHER A.,
RA DE SAINT BASILE G.;
RL NATURE 361:541-543(1993).
[10]
RX VARIANTS HIGM1 ARG-128; GLY-129 AND PRO-235.
RX MEDLINE; 93145330.
RA ARUFFO A., FARRINGTON M., HOLLENBAUGH D., LI X., MILATOVICH A.,
RA NONOYAMA S., BAJORATH J., GROSMAIRE L.S., STENKAMP R., NEUBAUER M.,
RA ROBERTS R.L., NOELLE R.J., LEDBETTER J.A., FRANCKE U., OCHS H.D.;
RL CELL 72:291-300(1993).
[11]
RX VARIANTS HIGM1 PRO-155; ASP-211 AND VAL-227.
RX MEDLINE; 93174270.
RA ALLEN R.C., ARMITAGE R.J., CONLEY M.E., ROSENBLATT H., JENKINS N.A.,
RA COPELAND N.G., BEDELL M.A., EDELHOFF S., DISTECHE C.M.,
RA SIMONEAUX D.K., FANSLW W.C., BELMONT J., SPRIGGS M.K.;
RL SCIENCE 259:990-993(1993).
[12]
RX VARIANTS HIGM1 ALA-126; ARG-140 AND GLU-144.
RX MEDLINE; 95233438.
RA MACCHI P., VILLA A., STRINA D., SACCO M.G., MORALI F., BRUGNONI D.,
RA GILIANI S., MANTUANO E., PASTH A., ANDERSSON B., ZEGERS B.J.M.,
RA CAVAGNI G., REZNICK I., LEVY J., ZAN-BAR I., PORAT Y., AIRO P.,
RA PLEBANI A., VEZZONI P., NOTARANGELO L.D.;
RL AM. J. HUM. GENET. 56:898-906(1995).
[13]
RX VARIANTS HIGM1 ARG-36; CYS-140; SER-231; MET-254 AND GLY-227 DEL.
RX MEDLINE; 97295077.
RA NONOYAMA S., SHIMADZU M., TORU H., SEYAMA K., NUNOI H., NEUBAUER M.,
RA YATA J.-I., OCH H.D.;
RL HUM. GENET. 99:624-627(1997).
CC -!- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
CC T-LYMPHOCYTES.
CC -!- DISEASE: DEFECTS IN CD40LG ARE THE CAUSE OF AN X-LINKED
CC IMMUNODEFICIENCY WITH HYPER-IGM (HIGM1), AN IMMUNOGLOBULIN ISOTYPE
CC SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM
CC IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES
CC PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE)
CC RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING
CC PNEUMOCYSTIS CARINII PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO
CC CRYPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH
CC INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR,
CC WITH A DEATH RATE OF ABOUT 10% BEFORE ADOLESCENCE.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -!- DATABASE: NAME-CD40Lbase; NOTE-European CD40L defect database;
CC WWW="http://www.expasy.ch/databases/cd40lbase.html";
CC FTP="ftp.expasy.ch/databases/cd40lbase".
DR EMBL; X68550; G37270; -
DR EMBL; X15017; G38484; -
DR EMBL; X67878; G38412; -
DR EMBL; L07414; G180124; -
DR EMBL; D31797; G1518170; -
DR EMBL; D31793; G1518170; JOINED.
DR EMBL; D31794; G1518170; JOINED.
DR EMBL; D31795; G1518170; JOINED.
DR EMBL; D31796; G1518170; JOINED.
DR PIR; S25684; S25684.
DR PIR; S26694; S26694.
DR PIR; S28017; S28017.
DR PIR; S28852; S28852.
DR PIR; JH0793; JH0793.
DR PDB; 1ALY; 17-SEP-97.
DR MM; 308230; -
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR; 3D-STRUCTURE;

DISEASE MUTATION. 22
KW DOMAIN 1
FT TRANSMEM 23
FT DOMAIN 47
FT DISULFID 178
FT CARBOHYD 240
FT VARIANT 36
FT VARIANT 123
FT VARIANT 126
FT VARIANT 128
FT VARIANT 140
FT VARIANT 140
FT VARIANT 140
FT VARIANT 144
FT VARIANT 155
FT VARIANT 211
FT VARIANT 227
FT VARIANT 227
FT VARIANT 231
FT VARIANT 235
FT VARIANT 254
SEQUENCE 261 AA; 29273 MW; DC2AD21F CRC32;
Query Match 7.2%; Score 165; DB 1; Length 261;
Best Local Similarity 29.5%; Pred. No. 8.25e-12;
Matches 44; Conservative 47; Mismatches 44; Indels 14; Gaps 12;
Db 122 IAAHVISEASKTTSVLQW-AEKGYTSLNNLVTLKNGKQLTVKRGQLYIYAQVTFCSN 180
QY 169 INAAISPGSHKVT-LSSWYHNRGWAKISN-M-TLSNGK-LRVNQDGFYIYANICF-RH 223
Db 181 REASSQAP--FIASL-CL-KSPGRF--ERILLRAANTHS-SAKPCGQ-QSIHLGGVPELQ 232
QY 224 HETSGSVPTDYQLQMLVYVVKTSIKIPSSHNLKMGSTKNWSEFHFYSINVGFFKL 283
Db 233 PGASVFNVTDPQSVSHGTGFTSFLGLKL 261
QY 284 AGEISIQVSNPSLLDPDQDATYFGAFKV 312
RESULT 7
ID CD4L BOVIN STANDARD; PRT; 261 AA.
AC PS1749;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39).
CD40LG OR CD40L.
OC BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; ARTIODACTYLA.
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE; 96006582.
RL MERTENS B.E.L.C.; MURIUKI M.; GAIDULIS L.;
RL IMMUNOGENETICS 42:430-431(1995).
CC -I- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -I- SUBUNIT: HOMOTRIMER.
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
DR EMBL; Z48469; G732570; -.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
FT DOMAIN 1
FT DISULFID 23
FT DOMAIN 47
FT DISULFID 178
FT DISULFID 218
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
M -> R (IN HGMI).
A -> E (IN HGMI).
V -> A (IN HGMI).
SE -> RG (IN HGMI).
W -> C (IN HGMI).
W -> G (IN HGMI).
W -> R (IN HGMI).
G -> E (IN HGMI).
L -> P (IN HGMI).
T -> D (IN HGMI).
G -> V (IN HGMI).
MISSING (IN HGMI).
L -> S (IN HGMI).
A -> P (IN HGMI).
T -> M (IN HGMI).
SEQUENCE 261 AA; 29273 MW; DC2AD21F CRC32;
Query Match 7.1%; Score 162; DB 1; Length 261;
Best Local Similarity 30.2%; Pred. No. 2.86e-11;
Matches 45; Conservative 40; Mismatches 50; Indels 14; Gaps 13;
Db 122 IAAHVISEASKTTSVLQW-APKGYTSLNNLVTLKNGKQLAVKRGQFYIYQVTFCSN 180
QY 169 INAAISPGSHKVT-LSSWYHNRGWAKISN-M-TLSNGK-LRVNQDGFYIYANICF-RH 223
Db 181 RETLSQAP--FIASL-CL-KSP-S-GSERILLRAANTHSSSKPCG-Q-QSIHLGGVPELQ 232
QY 224 HETSGSVPTDYQLQMLVYVVKTSIKIPSSHNLKMGSTKNWSEFHFYSINVGFFKL 283
Db 233 SGASVFNVTDPQSVSHGTGFTSFLGLKL 261
QY 284 AGEISIQVSNPSLLDPDQDATYFGAFKV 312
RESULT 8
ID TNFA_MOUSE STANDARD; PRT; 235 AA.
AC P06804;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNFA OR TNF.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
RP SEQUENCE FROM N.A.
RX MEDLINE; 88224564.
RA SHIRAI T.; SHIMIZU N.; SHIOJIRI S.; HORIGUCHI S.; ITO H.;
RL DNA 7:193-201(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85298296.
RA PENNICA D.; HAYFLICK J.S.; BRINGMAN T.S.; PALLADINO M.A.;
RA GOEDDEL D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 82:6060-6064(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86149365.
RA CAPUT D.; BEUTLER B.; HARTOG K.; THAYER R.; BROWN-SHIMER S.;
RA CERAMI A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 83:1670-1674(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85242112.
RA FRANSSEN L.; MULLER R.; MARMENOUT A.; TAVERNIER J.; VAN DER HEYDEN J.;
RA KAWASHIMA E.; CHOLLET A.; TIZARD R.; VAN HEUVERSWEIN H.; VAN VLIET A.;
RA RUYSSCHAERT M.-R.; FIERS W.;
RL NUCLEIC ACIDS RES. 13:4417-4429(1985).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87298639.
RA SHAKHOV A.N.; NEDOSPASOV S.A.;
RL BIOORG. KHIM. 13:701-705(1987).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88067722.
RA SEMON D.; KAWASHIMA E.; JONGENEEL C.V.; SHAKHOV A.N.; NEDOSPASOV S.A.;
RL NUCLEIC ACIDS RES. 15:9083-9084(1987).
RN [7]
RP SEQUENCE OF 80-99.
RX MEDLINE; 91097531.
RA SHERRY B.; JUC D.-M.; ZENTELLA A.; CERAMI A.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 173:1072-1078(1990).
RN [8]
RP SEQUENCE OF 70-87.
RX MEDLINE; 89380231.

mrg

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GN TNFA.
OS CAVIA PORCELLUS (GUINEA PIG) .
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-DUNKIN-HARTLEY;
RC STRAIN-HARTLEY; TISSUE-LUNG;
RA YUAN H.T., KELLY F.J., BINGLE C.D.;
RNL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-DUNKIN-HARTLEY;
RA WHITE A.M., YOSHIMURA T., SMITH A.W., WESTWICK J., WATSON M.L.;
RNL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS. IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
DR EMBL; U39839; G1066112; -
DR EMBL; U77036; G1679724; -
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
FT PROPEP 1 79
FT CHAIN 80 234
FT TRANSMEM 36 56
FT DISULFID 147 178
FT SEQUENCE 234 AA; 25793 MW; 00160783 CRC32;
SQ
Query Match 6.8%; Score 155; DB 1; Length 234;
Best Local Similarity 31.8%; Pred.No. 5.01e-10;
Matches 42; Conservative 28; Mismatches 50; Indels 12; Gaps

Db 106 WLKSRNALLANGGLSDNQLVVPDGLYLYSVLFKQ---GC-PS-YLLLTHTVSRL 160
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 WYHDRGWAKIS-MTLNSGKLRVNDGFFYYLANICFRHHTSGSVPTDYQLQMVYVKT 244
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 AVSYPEKVVLLSAIKSPCKEPEGAERKPVEPYLVGFGLOKQDRLSAEVNLPOYLD 220
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 245 SKIPSSNLM---KGGSTKNWSGNSEFH-FY-SINVGGFKLRAGEISIQVSNPSLLD 299
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 221 FADSGQIYFGVI 232
| : : : : :
QY 300 -PDQATYFGAF 310

RESULT 10
ID TNFA.RABIT STANDARD; PRT: 235 AA.
AC P04924;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN) .
GN TNFA.
OS ORYCTOLAGUS CUNICULUS (RABBIT) .
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; LAGOMORPHA.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 91065534.
RA SHAKHOV A.N., KUPRASH D.V., AZIZOV M.M., JONGENEEL C.V.

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RA NEDOSPASOV S.A.;
 RL GENE 95:215-221(1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 86219712.
 RA ITO H., SHIRAI T., YAMAMOTO S., AKIRA M., KAWAHARA S., TODD C.W.,
 RA WALLACE R.B.;
 RL DNA 5:157-165(1986).
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 86219711.
 RA ITO H., YAMAMOTO S., KURODA S., SAKAMOTO H., KAJIHARA J., KIYOTA T.,
 RA HAYASHI H., KATO M., SEKO M.;
 RL DNA 5:149-156(1986).
 RN [3]
 CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
 CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
 CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
 CONDITIONS.
 CC -!- SUBUNIT: HOMOTRIMER.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 EXTRACELLULAR SOLUBLE FORM.
 CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 PROTEOLYTIC PROCESSING.
 CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 AND MALNUTRITION.
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 DR EMBL; M12845; G165760; -;
 DR EMBL; M12846; G165753; -;
 DR EMBL; M60340; G165756; -;
 DR PIR; A25451; A25451.
 DR PIR; A25454; A25454.
 DR PIR; JS0727; JS0727.
 DR HSP; P01375; ITNF.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 KW CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
 FT PROPEP 1 79
 FT CHAIN 80 235 TUMOR NECROSIS FACTOR.
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DISULFID 148 179 BY SIMILARITY.
 FT CONFLICT 63 63 MISSING (IN REF. 3).
 SQ SEQUENCE 235 AA; 25816 MW; 1BC5CD8 CRC32;
 Query Match 6.6%; Score 152; DB 1; Length 235;
 Best Local Similarity 26.0%; Pred. No. 1.68e-09;
 Matches 33; Conservative 33; Mismatches 55; Indels 6; Gaps 6;
 Db 107 WLSORANALLANGMKLTDNQLVWPADGLYLYSOVLFGSGGCRSVLLTH-TVSRFAVSY 165
 QY 186 WYHGRGWAKISN-MTLNKGKLRVQDGYLYANICFRHHTSGSVPTDYQLQMLVYVKT 244
 Db 166 PNKV-NLLSAIKSPCHRETPPEAEPMWYEPYILGGVFQLEKGRDLSTEVNOPEYLDLAE 224
 QY 245 SIKIPSSHNLKMGSTKNWGNSE-FHEY-SINVGFFKLRAGEISIQVSNPSLLD-PD 301
 Db 225 SGQVYFG 231
 QY 302 QDATYFG 308
 RESULT 11
 ID TNFA_RAT STANDARD; PRT; 235 AA.
 AC P16599;
 DT 01-AUG-1990 (REL. 15, CREATED)
 DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
 GN TNFA.
 OS -RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=TESTIS;
 RX MEDLINE; 94040766.
 RA KWON J., CHUNG I.Y., BENVENISTE E.N.;
 RL GENE 132:227-236(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RA SHIRAI T., SHIMIZU N., HORIGUCHI S., ITO H.;
 RL AGRIC. BIOL. CHEM. 53:1733-1736(1989).
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 92329007.
 RA ESTLER H.C., GREWE M., GAUSSLING R., PAVLOVIC M., DECKER K.;
 RL BIOL. CHEM. HOPPE-SEYLER 373:271-281(1992).
 RN [4]
 CC SEQUENCE OF 1-231 FROM N.A.
 RC TISSUE-TAIL;
 RA KIRISITS M.J., VARDIMON D., KUNZ H.W., GILL T.J. III;
 RL SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
 CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
 CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
 CONDITIONS.
 CC -!- SUBUNIT: HOMOTRIMER.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 EXTRACELLULAR SOLUBLE FORM.
 CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 PROTEOLYTIC PROCESSING.
 CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 AND MALNUTRITION.
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 DR EMBL; X66539; G395370; -;
 DR EMBL; L00981; G205254; -;
 DR EMBL; D00475; G220921; -;
 DR EMBL; L19123; G310232; -;
 DR PIR; JU0029; JU0029.
 DR PIR; S21674; S21674.
 DR PIR; JN0868; JN0868.
 DR HSP; P01375; ITNF.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 KW CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
 FT PROPEP 1 79
 FT CHAIN 80 235 TUMOR NECROSIS FACTOR.
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DISULFID 148 179 BY SIMILARITY.
 FT CARBOHYD 86 86 POTENTIAL.
 FT CONFLICT 39 39 L -> P (IN REF. 3).
 FT CONFLICT 163 163 I -> T (IN REF. 3).
 FT CONFLICT 202 202 F -> S (IN REF. 3).
 SQ SEQUENCE 235 AA; 25806 MW; CIDF18B7 CRC32;
 Query Match 6.5%; Score 150; DB 1; Length 235;
 Best Local Similarity 25.6%; Pred. No. 3.76e-09;
 Matches 33; Conservative 32; Mismatches 58; Indels 6; Gaps 6;
 Db 107 WLSORANALLANGMDLKNQLVVVPADGLYLYSQVLFGKQCPDYVLLTH-TVSRFAISY 165
 QY 186 WYHGRGWAKISN-MTLNKGKLRVQDGYLYANICFRHHTSGSVPTDYQLQMLVYVKT 244
 Db 166 QEKV-SLLSAIKSPCKDTPEGAELKFWPEWYILGGVFQLEKGDLLSAEYNLPKYLITE 224
 QY 245 SIKIPSSHNLKMGSTKNWGNSEF-FY-SINVGFFKLRAGEISIQVSNPSLLD-PD 301
 Db 225 SGQVYFGVI 233
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QY 302 QDNTYGFAG 310

RESULT 12
ID CD4L MOUSE STANDARD; PRT; 260 AA.
AC P27548;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39).
DE GN CD40LG OR CD40L.
DE OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 92244364.
RX ARMITAGE R., FANSLON W., SATO T.A., CLIFFORD K.N., STROCKBINE L., MACDOUFF B.M., ANDERSON D.M., GIMPEL S.D., DAVIS-SMITH T., MALISZEWSKI C.R., CLARK E.A., SMITH C.A., GRABSTEIN K.H., COSMAN D., SPRIGGS M.K.;
RX NATURE 357:80-82(1992).
RN [2]
RN SIMILARITY TO THE TNF FAMILY.
RX MEDLINE: 93200072.
RX PEITSCH M.C., JONGENEEL C.V.;
RN INT. IMMUNOL. 5:233-238(1993).
CC -I- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4. INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
CC -I- SUBUNIT: HOMOTRIMER.
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS EXTRACELLULAR SOLUBLE FORM.
CC -I- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+ T-LYMPHOCYTES.
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY. EMBL: X65453; G50352; -.
DR PIR: S21738; S21738.
DR PDB: LCDA; 3I-OCT-93.
DR MGD: MGI:88337; CD40L.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR; 3D-STRUCTURE. DOMAIN1 1 22 CYTOPLASMIC (POTENTIAL).
DR TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 47 260 EXTRACELLULAR (POTENTIAL).
FT DISULFID 177 217 POTENTIAL.
FT CARBOHYD 239 239
FT SEQUENCE 260 AA; 29396 MW; 420FF8C9 CRC32;

Query Match 6.5%; Score 150; DB 1; Length 260;
Best Local Similarity 29.6%; Pred. No. 3.76e-09;
Matches 48; Conservative 49; Mismatches 47; Indels 18; Gaps

Db 113 ORGDEDPQIAHV-VSEAN-SNAA-SV-LQ-W-AKKGYTNKSNLWMLNGKOLTYVREG 16
QY 155 QRGKPAQPFALHTLINAASIPSGSHKVTLSWYHDGW-AKISNMT-LSNGK-LRVNQDG 21
Db 167 LYVYVTVTFCSNREPSSOR--FT-VGLWL-KPSI--GSERILLKAANTHSSSQLE-Q 21
QY 212 FYLYXANICF-RHETSGSVPTDYLQLVVYVVKYSIKTPSHNLKMGKSTKNSGSEPH 27
Db 220 -QSVHLGVFELQAGSAFVNVTASQVYHVRVGFSSFGLKL 260
QY 271 FYGINVGGFKLRAGEISIQVSNPSLLDPQDATYFCFAKV 312

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DR EMBL; UI12029; G515509; -
DR EMBL; UI6984; G577432; -
DR EMBL; UI6985; G577831; -
DR EMBL; U06950; G495466; -
DR MGD; MGI:104796; LTB;
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
FT DOMAIN 1 27 CYTOPLASMIC (POTENTIAL).
FT FT MEMEM 28 48 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 49 306 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 98 98 POTENTIAL.
FT CARBOHYD 284 284 POTENTIAL.
SQ SEQUENCE 306 AA; 32328 MW; 7C9780D1 CRC32;

Query Match          5.98; Score 136; DB 1; Length 306;
Best Local Similarity 28.7%; Pred. No. 9.04e-07;
Matches 33; Conservative 28; Mismatches 47; Indels 7; Gaps 6

Db      191 LALPDQGVVLYCHVGVRGTPAGRSRLTSRALYRAGGAYGRGSPPELLLEGAETV 250
        | : ||| |||| :: :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY      205 LRVNQDGFFLYLANICFR-HHETSQSVPTDYQLM--VYVVVKSIKIPSSHNLMKGSTK 261
        :: :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db      251 TPVVDITGYSLMTVSYGFGLAQLRSGERYVYNISHDPMDVYRRGRTFFGAVMV 305
        :: :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY      262 NWSGNS-EF-HF-Y-SINVGGFFKL RAGEISIQVSNPSLLDDPDQATYFGAFKV 312

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W P E R F H (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Nov 13 17:16:46 1998; Maspar time 19.37 Seconds
812.531 Million cell updates/sec
Circular output not generated.

Title: >US-08-989-362-2
Description: (1-316) from US08989362.pep
Perfect Score: 2294
Sequence: 1 MRRASRDYKYLRSSEMGSG.....LLDPDQDQTYFGAFKVDID 316

Scoring table: PAM 150
Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrmbl6
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 46.565; Variance 93.226; scale 0.499

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2294	100.0	316	11	035235	0.00e+00
2	2287	99.7	316	11	035306	0.00e+00
3	1986	86.6	317	4	014788	0.00e+00
4	1527	66.6	245	4	014723	5.51e-284
5	175	7.6	279	11	061217	1.58e-11
6	160	7.0	232	11	035853	3.97e-09
7	161	7.0	233	11	035734	2.76e-09
8	152	6.6	156	11	062326	7.03e-08
9	148	6.5	240	4	043557	2.89e-07
10	142	6.2	234	6	028320	2.35e-06
11	125	5.4	216	11	070332	7.11e-04
12	123	5.4	233	6	018779	1.36e-03
13	122	5.3	157	4	043647	1.88e-03
14	120	5.2	1055	11	054967	3.56e-03
15	106	4.6	348	6	002755	2.64e-01
16	105	4.6	375	10	P93066	3.54e-01
17	106	4.6	642	2	Q55103	2.64e-01
18	104	4.5	1091	4	Q70912	4.75e-01
19	100	4.4	200	13	Q73770	1.50e+00
20	101	4.4	223	8	Q34914	1.13e+00

21	100	4.4	223	8	Q34861	1.50e+00
22	100	4.4	223	8	Q34885	1.50e+00
23	100	4.4	223	8	Q34932	1.50e+00
24	100	4.4	223	8	Q34933	1.50e+00
25	100	4.4	223	8	Q34871	1.50e+00
26	100	4.4	232	7	Q31553	1.50e+00
27	100	4.4	263	13	Q73896	1.50e+00
28	100	4.4	263	7	Q31410	1.50e+00
29	100	4.4	286	7	Q31413	1.50e+00
30	100	4.4	473	11	Q63887	1.50e+00
31	101	4.4	4436	1	Q58659	1.13e+00
32	98	4.3	520	11	Q61078	2.64e+00
33	99	4.3	657	11	Q35391	1.99e+00
34	99	4.3	663	5	Q61317	1.99e+00
35	99	4.3	1616	4	Q15054	1.99e+00
36	96	4.2	160	8	Q21745	4.60e+00
37	97	4.2	223	8	Q34899	4.60e+00
38	96	4.2	223	8	Q34906	4.60e+00
39	96	4.2	223	8	Q34934	4.60e+00
40	96	4.2	223	8	Q34924	4.60e+00
41	97	4.2	1217	5	Q17889	3.49e+00
42	97	4.2	1343	14	Q06635	3.49e+00
43	97	4.2	5071	5	P91905	3.49e+00
44	97	4.2	5107	5	Q94279	3.49e+00
45	96	4.2	5262	4	Q14686	4.60e+00

ALIGNMENTS

RESULT 1
ID O35235 PRELIMINARY: PRT; 316 AA.
AC O35235;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE TRANCE.

OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97460112.
RA WONG B.R., RHO J., ARRON J., ROBINSON E., ORLINICK J., CHAO M.,
RA KALACHIKOV S., CAYANI E., BARTLETT F.S. III, FRANKEL W.N., LEE S.Y.,
RA CHOI Y.;
RL J. BIOL. CHEM. 272:25190-25194(1997).
RN [2]
RP SEQUENCE FROM N.A.

RA LACEY D.L., TIMMS E., TAN H.-L., KELLEY M.J., DUNSTAN C.R.,
RA BURGESS T., ELLIOTT R., COLOMERO A., ELLIOTT G., SCULLY S., HSU H.,
RA SULLIVAN J., HAWKINS N., DAVY E., CAPPARELLI C., ELI A., QIAN Y.-X.,
RA KAUFMAN S., SAROSI I., SHALHOUB V., SENALDI G., GUO J., DELANEY J.,
RA BOYLE W.J.;
RL CELL 93:165-176(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW;
RA YASUDA H., SHIMA N., NAKAGAWA N., YAMAGUCHI K., KINOSAKI M.,
RA MOCHIZUKI S., TOMOYASU A., YANO K., GOTO M., MURAKAMI A., TSUDA E.,
RA MORINAGA T., HIGASHIO K., UDAGAWA N., TAKAHASHI N., SUDA T.;
RL PROC. NATL. ACAD. SCI. U.S.A. 95:3597-3602(1998).
DR EMBL; AF013170; G2411498;
DR EMBL; AF053713; G3057148;
DR EMBL; AB008426; D1026353;
DR PFAM; PF00229; TNF.
SQ SEQUENCE 316 AA; 34944 MW; F76EC806 CRC32;

Query Match 100.0%; Score 2294; DB 11; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MRRASRDYKYLRSSEMGSGCPVHEGPHAPSPAPAPPPAASRSMFLALGLG 60
|||||

Qy	1	MRRASRDYGYKLRSSEMGSGPGVHEGPHUPAPAPAPAPPAAASRWFLLALLGLUGLQG	60
Db	61	VVCSIALFLYFRAQMDPNRISEDTHCFYRILRLHENAGLQDSTLSEDTLPDSCRRMKQ	120
Qy	61	VVCSIALFLYFRAQMDPNRISEDTHCFYRILRLHENAGLQDSTLSEDTLPDSCRRMKQ	120
Db	121	AFQGAVOKELOHIVGPORFSGAPAMWEGSWLDVAQKGPAPQFAHLTINAAASIPSGSHK	180
Qy	121	AFQGAVOKELOHIVGPORFSGAPAMWEGSWLDVAQKGPAPQFAHLTINAAASIPSGSHK	180
Db	181	VTLSWSYHDRGWAKISNMTLSNGKLRVNQDGFYLLYANICFRHHTSGSVPTDYLQLMWY	240
Qy	181	VTLSWSYHDRGWAKISNMTLSNGKLRVNQDGFYLLYANICFRHHTSGSVPTDYLQLMWY	240
Db	241	VVKTSIKIPSSHNLKMGSTKNNSGNSEFHFSYINVGGFKKRAGEEISIQVSNPSSLDP	300
Qy	241	VVKTSIKIPSSHNLKMGSTKNNSGNSEFHFSYINVGGFKKRAGEEISIQVSNPSSLDP	300
Db	301	QDQATYFQAFKVQDID 316	
Qy	301	QDQATYFQAFKVQDID 316	

[illegible]

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RESULT 3
ID O14788 PRELIMINARY; PRT; 317 AA.
AC O14788;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE RANKL.
GN RANKL.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAOGA; CHORDATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98032977.
RA ANDERSON D.M., MARASKOVSKY E., BILLINGSLEY W.L., DOUGALL W.C.,
RA TOMESKO M.E., ROUX E.R., TEEPE M.C., DUBOSE R.F., COSMAN D.,
RA GALIBERT L.;
RL NATURE 390:175-179(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA LACEY D.L., TIMMS E., TAN H.-L., KELLEY M.J., DUNSTAN C.R.,
RA BURGESS T., ELLIOTT R., COLOMBO A., ELLIOTT G., SCULLY S., HSU H.,
RA SULLIVAN J., HAWKINS N., DAVY E., CAPARELLI C., ELI A., QIAN Y.-X.,
RA KAUFMAN S., SAROSI I., SHALHOUB V., SENAUDI G., GUO J., DELANEY J.,
RA BOYLE W.J.;
RL CELL 93:165-176(1998).
DR CELL; AF019047; G2612922; -.
DR EMBL; AF019047; G2612922; -.
DR EMBL; AF053712; G3057146; -.
DR PFAM; PF00229; TNF.
DR PFAM; PF00229; TNF.
SQ SEQUENCE 317 AA; 35478 MW; A58E6DC4 CRC32;

Query Match 86.6%; Score 1986; DB 4; Length 317;
Best Local Similarity 84.6%; Pred. No. 0.00e+00;
Matches 269; Conservative 30; Mismatches 16; Indels 3; Gaps 3;

Db 1 MRRASRDYTKYLRSEEMGGPGAPHEGPLH-APPPAPHPQPAASRSMFVALLGLGQ 59
Qy 1 MRRASRDYTKYLRSEEMGGPGVPEHGPLHPAPAPAPPAAASRSMFVALLGLGQ 60
Db 60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADQDTTLESQDTKLIPDSCRI 119
Qy 61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLDSTLESDI-L-PDSCRM 118
Db 120 KQAFQGVQKELQHVQSHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATIPSGS 179
Qy 119 KQAFQGVQKELQHVQSPFGAPAMMGESWLDVAQRGPXAQPFALHTINAASIPSGS 178
Db 180 HKVLSLWYHDRGWAKISNTFSGKLIVNODGFYILYANICFRHHETSGDLATEYLQM 239
Qy 179 HKVLSLWYHDRGWAKISNTLSNGKRVQDGFYILYANICFRHHETSGSVPTDYQLM 238
Db 240 VYVTKTSIKIPSSHTLMKGSTKYWNSGFHYISVNGVGFYKLRSGEEISIEVSNPSLL 299
Qy 239 VYVTKTSIKIPSSHNLKMGSTKNWNSGFHYISVNGVGFYKLRSGEEISIEVSNPSLL 298
Db 300 DPQDQATYFGAFKVRDID 317
Qy 299 DPQDQATYFGAFKVRDID 316

RESULT 4
ID O14723 PRELIMINARY; PRT; 245 AA.
AC O14723;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE TRANCE (FRAGMENT).
GN TRANCE.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAOGA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE; 97460112.
RA WONG B.R., RHO J., ARRON J., ROBINSON E., ORLINICK J., CHAO M.,
RA KALACHIKOV S., CAYANI E., BARTLETT F.S. III, FRANKEL W.N., LEE S.Y.,
RA CHOI Y.,
RL J. BIOL. CHEM. 272:25190-25194(1997).
DR EMBL; AF013171; G2411500; -.
DR PFAM; PF00229; TNF.
FT NON_TER 1
SQ SEQUENCE 245 AA; 27804 MW; F7CD1ECE CRC32;

Query Match 66.6%; Score 1527; DB 4; Length 245;
Best Local Similarity 84.5%; Pred. No. 5.51e-284;
Matches 207; Conservative 24; Mismatches 12; Indels 2; Gaps 2;

Db 1 QMDPNRISDGTGTCIYRILRLHENDQDTTLESDQDTKLIPDSGRIRKQAFQAVQKELQ 60
QY 74 QMDPNRISDGTGTCIYRILRLHENDQDTTLESDQDTKLIPDSGRIRKQAFQAVQKELQ 131
Db 61 HYGVSQHIRAEKAMVDGSLDLAKRSLEAOPFAHLTINATDIPSGSHKVSLSWYHDSRG 120
132 HYGVPQSFESAPAMWESWLDVARGPEAOPFAHLTINAAISFGSHKVTLSWYHDSRG 191
Db 121 WGSINMTFSGKLVNQDGFYLYANICFRHETSGDLATEYLQLMVYVTKTSIKIPSS 180
QY 192 WAKISNMTLSNGKLVNQDGFYLYANICFRHETSGSVPTDYQLQLMVYVTKTSIKIPSS 251
Db 181 HTLMKGSTYWSGNSSEFHFYSINVGFFKLRSGEETISIEVSNPSLLDPDQDATYFGAFK 240
QY 252 HNLKMGSTYWSGNSSEFHFYSINVGFFKLRSAGEETISIQVSNPSLLDPDQDATYFGAFK 311
Db 241 VRDID 245
QY 312 VQDID 316

RESULT 5
ID O61217 PRELIMINARY; PRT; 279 AA.
AC Q61217;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE FAS LIGAND.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=BALE/C;
FENNER M.H., SHIODA T., ISSELBACHER K.J.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U58995; G1389772; -.
DR PROSITE; PS00251; TNF_1; 1.
DR PFAM; PF00229; TNF.
SQ SEQUENCE 279 AA; 31340 MW; 9062DF08 CRC32;

Query Match 7.6%; Score 175; DB 11; Length 279;
Best Local Similarity 25.9%; Pred. No. 1.58e-11;
Matches 35; Conservative 40; Mismatches 52; Indels 8; Gaps 7;

Db 153 SRISPLE-WEDTGTALISGVYKKGGLVINEAGLYFYYSKVYRQ-SCNNQPLN--H- 207
QY 178 SHKVTLSWYHDSRGWAKISNMTLSNGKLVNQDGFYLYANICFRHETSGSVPTDYQLQ 237
Db 208 KYVM-RNS-KYPGLVLMSEKRL-NYCTTGQIWAHSSYLGVAFNLTSADHYLVNISQLSL 264
+QY 238 MVYVVKTSIKIPSSHNLKMGSTKNWGSNSEFHFYSINVGFFKLRSAGEETISIQVSNPSL 297
Db 265 INFEEKSTFFGLVKL 279
QY 298 LDPDQDATYFGAFK 312
RESULT 6

ID O35853 PRELIMINARY; PRT; 232 AA.
AC O35853;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR ALPHA.
GN TNFA.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE; 97246744.
RA IRAQI F., TEALE A.;
RL IMMUNOGENETICS 45:459-461(1997).
DR EMBL; U68414; G2304957; -.
DR PROSITE; PS00251; TNF_1; 1.
DR PFAM; PF00229; TNF.
SQ SEQUENCE 232 AA; 25513 MW; 9B2B3F06 CRC32;

Query Match 7.0%; Score 160; DB 11; Length 232;
Best Local Similarity 25.6%; Pred. No. 3.97e-09;
Matches 33; Conservative 34; Mismatches 56; Indels 6; Gaps 6;

Db 104 WLSQRANALLANGMDLKNQLVVPADGLYVYQVLFKQGCQPDYVLLTH-TVSRFAISY 162
QY 186 WYHDSRGWAKISN-MTLSNGKLVNQDGFYLYANICFRHETSGSVPTDYQLQLMVYVVK 244
Db 163 QEKV-NLLSAVSPCKDTPGEAELKPWTEPIYLGVSFQLEKGDLSAEVNLKPYLDFAE 221
QY 245 STKIPSSHNLKMGSTKNWGSNSEFHFY-SINVGFFKLRSAGEETISIQVSNPSLLD-PD 301
Db 222 SGQVYFGVI 230
QY 302 QDATYFGAF 310

RESULT 7
ID O35734 PRELIMINARY; PRT; 233 AA.
AC O35734;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR ALPHA PRECURSOR.
GN TNF-ALPHA.
OS MARMOTA MONAX (WOODCHUCK).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PBMC;
RA LOHRENGEL B., LU M., ROGGENDORF M.;
RL IMMUNOGENETICS 47:332-335(1998).
DR EMBL; Y14137; E348344; -.
DR PROSITE; PS00251; TNF_1; 1.
DR PFAM; PF00229; TNF.
KW SIGNAL.
FT SIGNAL 1 77 POTENTIAL.
FT CHAIN 78 233 POTENTIAL.
SQ SEQUENCE 233 AA; 25764 MW; 6FC0F34A CRC32;

Query Match 7.0%; Score 161; DB 11; Length 233;
Best Local Similarity 26.2%; Pred. No. 2.76e-09;
Matches 37; Conservative 34; Mismatches 63; Indels 7; Gaps 7;

Db 94 VAKNEDKEQLV-WLSRRANALLANGMELDNQLVVPANGLYVYQVLFKQGCQPSVLL 152
QY 174 IPSGSHKVTLSWYHDSRGWAKISN-MTLSNGKLVNQDGFYLYANICFRHETSGSVPT 232
Db 153 TH-TVSRFAISYQDKV-NLLSAKSPCKESLEGAEFKPWTEPIYLGVSFQLEKGDRLSA 210
QY 233 DYQLQLMVYVVKTSIKIPSSHNLKMGSTKNWGSNSEFHFY-SINVGFFKLRSAGEETIS 290

Db 211 EVNLPSYLDFAESGQVVFVI 231
:|: || || :: ||| :
QY 291 QVSNPSLLD-PDQDATYFGAF 310

RESULT 8
ID Q62326 PRELIMINARY; PRT; 156 AA.

QC2326;	AC	01-NOV-1996	(TREMBLREL. 01, CREATED)
01-NOV-1996	AC	(TREMBLREL. 01, LAST SEQUENCE UPDATE)	
01-JUN-1998	DT	(TREMBLREL. 06, LAST ANNOTATION UPDATE)	
TUMOR NECROSIS FACTOR.	DT		
MUS MUSCULUS (MOUSE).	DE		
EUKARYOTA; METAZOA;	OS		
EUTHERIA; RODENTIA.	OS		
[1]	OC		
SEQUENCE FROM N.A.	RN		
MEDLINE; 86149365.	RP		
CAPUT D., BEUTLER B.,	RX		
ARTOG K., BROWN-SHIMER S.,	RA		
GERAMI A.;	RA		
PROC. NATL. ACAD. SCI. U.S.A. 83:1670-1674(1986).	RA		
EMBL; M13049; E7693; -	DR		
PROSITE; PS00251; TNF_1; 1.	DR		
PFAM; PF00229; TNF.	DR		
SEQUENCE 156 AA; 17357 MW	SO		
03975542 CRC32:			

Query Match 6.6%; Score 152; DB 11; Length 156;
Best Local Similarity 25.4%; Pred. No. 7.03e-08;
Matches 32: Conservative 33: Mismatches 55: Indels

Db	28	WLSORANALLANGMDLKDNLVVPADGLXYLVYSQVLFKGGCPDYVLLTH-TVSREFAISY	86
		: : : : : : : : : : : : : : :	
QY	186	WYHDRGWAKISN-MTLNSGKLRYNQDGFYYLIYANICFRHETSGSYPTDYLQLMVVVXT	244
		: : : : : : : : : : : : : : :	
Db	87	QEKV-NULSAVKSPCKDTPGEAELKPWTPEIYLGGVFOLEKGDLGSAEYNLPKYLDFAE	145
		: : : : : : : : : : : : : : :	
QY	245	SIKIPSSHMLMKGSTKNWSGNSEFH-FY-SINVGFFKLRACEEITSIQVSNPSLDD-PD	301
		: : : : : : : : : : : : : : :	
Db	146	SGQVYF	151
QY	302	QDATYF	307

RESULT 9
ID 043557
PRELIMINARY:
PRT: 240 AA.

AC	043557:	
DT	01-JUN-1998 (TREMREL. 06, CREATED)	
	01-JUN-1998 (TREMREL. 06, LAST SEQUENCE UPDATE)	
DE	01-JUN-1998 (TREMREL. 06, LAST ANNOTATION UPDATE)	
OS	TUMOR NECROSIS FACTOR SUPERFAMILY MEMBER LIGHT.	
OS	HOMO SAPIENS (HUMAN).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	MAURI D.N., EISNER R., MONTGOMERY R.I., KOCHEL K.D., CHEUNG T.C.,	
RA	YU G.-L., RUBEN S., MURPHY M., EISENBERG R.J., COHEN G.H., SPEAR P.G.,	
RA	WARE C.F.;	
RL	IMMUNITY 8:21-30(1998).	
DR	EMBL; AF036581; G2813624; -	
SQ	SEQUENCE 240 AA; 26351 MW; 4A4B603A CRC32;	

Query Match 6.5%; Score 148; DB 4; Length 240;

Best Local Similarity 27.2%; Pred. No. 2.89e-07;
Matches 46; Conservative 42; Mismatches 71; Indels 10; Gaps 10;

[illegible]

QY	207	VNODGFYLLYANICFRHHETSGSVPTDYLQLVVVVVKTSIKIPSSHNLMKGGSTK-NWSG	265
Db	192	SSSRVWDDSFGLGVHLEAGEEYVVRVLDRLVRLRDGTRSYFGAFV	240
QY	266	NSEFHFYISIN-VGGFFFKLRAGEISIQVNSPLD-PDODATYFGAFV	312

RESULT 10
ID Q28320
PRELIMINARY:
PRT: 234 AA.

AC	Q28320;	
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)	
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DT	01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)	
DE	TNF-ALPHA.	
OS	CAPRA HIRCUS (GOAT).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; ARTIODACTYLA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	RAKAKURA H., MORI Y., TATSUMI M.;	
RL	SUBMITTED (JUL-1996) TO ENBL/GENBANK/DBJ DATA BANKS.	
DR	ENBL: D86587; G1483165; "	
DR	PROSITE; PS00251; TNF_1; 1.	
DR	PFAM; PF00229; TNF.	
SQ	SEQUENCE 234 AA; 25519 MW; C6424744 CRC32;	

Query Match 6.2%; Score 142; DB 6; Length 234;
Best Local Similarity 23.8%; Pred. NO. 2.35e-06;
Matches 43; Conservative 48; Mismatches 80; Indels

Db	55	VIGPQREEQSPAGPSFNRLPVQTLRRSSQASSNKPVAHVVANTISAPQO-LRWGDSYAN-A	112
Qy	133	IVGPQRESGAPAMMEGSW-LDVAQRGPEAOPFAHLITINAASIPSGSHKVTLLSSWYHDRG	191
Db	113	-LKANGVELKDNQLVPTDGLYLIYSOVLPRHGCP-STPL-FLTWITISRIAVSYOTKVN	169
Qy	192	WAKISNNMTLSGKLRVNQDGFYLLYANICPRHHETSGSVPTDYQLMWVYVKTSIKIPSS	251
Db	170	ILSAIKSPCHRETPGEAEAKPTWETPIYQGVFTQLEKGRDLRSAINOPEYLDYAESGVTF	229
Qy	252	-HNLMKGSTKNWNSGSEFH-FY-SINVGFFKLRAGEIISIQVSNPSLLD-PDQDATVF	307

RESULT	11
ID	070332

AC	070332:	
AD	01-AUG-1998 (TREMBLEL. 07, CREATED)	
AE	01-AUG-1998 (TREMBLEL. 07, LAST SEQUENCE UPDATE)	
AF	01-AUG-1998 (TREMBLEL. 07, LAST ANNOTATION UPDATE)	
AG	01-AUG-1998 (TREMBLEL. 07, LAST SEQUENCE UPDATE)	
AH	TUMOR NECROSIS FACTOR-ALPHA (FRAGMENT).	
AI	TUMOR NECROSIS FACTOR-ALPHA (FRAGMENT).	
AJ	MESOCIRCEPUS AURATUS (GOLDEN HAMSTER).	
AK	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; E	
AL	EUTHERIA; RODENTIA.	
AM	[1]	
AN	SEQUENCE FROM N.A.	
AO	RP	
AP	TISSUE-SPLEEN.	
AQ	MELEY P.C., TRYON V. V., CHANDRASEKAR B., FREEMAN G.L.;	
AR	INFECT. IMMUN. 66:2135-2142(1998).	
AS	EMBL; AF046215; G3005109; -.	
AT	PROSITE; PS00251; TNF_1; 1.	
AV	NON_TER	1
AW	NON_TER	1
AX	NON_TER	216
AY	SEQUENCE	216 AA; 23793 MW; 79A08367 CRC32;
AZ		

Query Match 5.4%; Score 125; DB 11; Length 216;
Best Local Similarity 29.2%; Pred. No. 7.11e-04;

Db 97 WLSHRANALLANGMSLKDNQLVIPADGLYLVYSQVLFGRQ---GC-PS-YVLLTHTVSRI 151

QY 186 WYHGRGWAKISN-MTSLNGKLRVNDQGFYLYANICFRHHETSGSVPTDYLQLVVYVK 244
 Db 152 AVSYEDVNLLSAIKSPCPKETEGELKPWYEPYIYGGVFOLEKGRDLGSAEINLPYLD 211
 QY 245 SIKIPSSHNLNLM--KGGSTKNWGSNEFH-FY-SINVGFFKLKRAGEISIQVSNPSLLD 299

RESULT 12
 ID O18779 PRELIMINARY; PRT; 233 AA.
 AC O18779;
 DT 01-JAN-1998 (TREMBREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR ALPHA.
 GN TNFA.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 [1]
 SEQUENCE FROM N.A.
 STRAIN-N'DAMA;
 RA IRAQI F.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AF011926; G2599343;
 DR PROSITE; PS00251; TNF_1; 1.
 DR PFAM; PF00229; TNF.
 SQ SEQUENCE 233 AA; 25395 MW; 64FAFC88 CRC32;

Query Match 5.4%; Score 123; DB 6; Length 233;
 Best Local Similarity 25.2%; Pred. No. 1.36e-03;
 Matches 32; Conservative 29; Mismatches 61; Indels 5; Gaps 5;

Db 104 WDSYANALMANGVKLEDNOLVVPADGLYIYQVLFKGGCPSTPLFLTHTSIRIAVS 163
 QY 186 WYHGRGWAKISN-MTSLNGKLRVNDQGFYLYANICFRHHE-TSGSV-PTDYLQLVVYV 242
 Db 164 QTKVNLSAISKCHRETPPEWAKPM-YEPIYQVFOLEKGRDLGSAEINLPYLDYAE 222
 QY 243 KTSIKIPSSHNLKGGSTKNWGSNEFHYSINVGFFKLKRAGEISIQVSNPSLLD-PD 301

Db 223 SGQVYFG 229
 QY 302 QDATYFG 308

RESULT 13
 O43647 PRELIMINARY; PRT; 157 AA.
 O43647;
 DT 01-JUN-1998 (TREMBREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBREL. 06, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBREL. 06, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).
 GN TNFA.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 [1]
 SEQUENCE FROM N.A.
 RA JANG J.S., KIM B.E.;
 RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AF043342; G2905634;
 DR PROSITE; PS00251; TNF_1; 1.
 FT NON_TER 1
 SQ SEQUENCE 157 AA; 17380 MW; FD78F0A6 CRC32;

Query Match 5.3%; Score 122; DB 4; Length 157;
 Best Local Similarity 24.2%; Pred. No. 1.88e-03;
 Matches 31; Conservative 32; Mismatches 58; Indels 7; Gaps 7;
 Db 28 WLNRRNALIANGLVLRDNLVVPSEGLYIYQVLFKGGCPSTHLLTHTSIRI-AVS 86
 QY 186 WYHGRGWAKISN-MTSLNGKLRVNDQGFYLYANICFRHHE-TSGSVPTDYLQLVVYVK 243

Db 87 YQTKV-NLLSAIKSPCQRETPRGAFAKWPYEPYIYGGVFOLEKGRDLGSAEINRPDYLDA 145
 QY 244 TSIKIPSSHNLKGGSTKNWGSNEFH-FY-SINVGFFKLKRAGEISIQVSNPSLLD-P 300
 Db 146 ESGQVYFG 153
 QY 301 QDATYFG 308

RESULT 14
 ID O54967 PRELIMINARY; PRT; 1055 AA.
 AC O54967;
 DT 01-JUN-1998 (TREMBREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBREL. 06, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)
 DE NON-RECEPTOR PROTEIN TYROSINE KINASE ACK.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 [1]
 SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA HER J.-H., BOLEN J.B.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AF037260; G2921447;
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 SQ SEQUENCE 1055 AA; 116834 MW; F1AB2646 CRC32;

Query Match 5.2%; Score 120; DB 11; Length 1055;
 Best Local Similarity 40.5%; Pred. No. 3.56e-03;
 Matches 17; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

Db 887 YQRLREAQSFEPAALP-VPPLPPSTPAPAPATATVRPM 927
 QY 8 YGYLRSEEMSGSGVPGHPGLHPAPAPAPPPAASRSM 49

RESULT 15
 ID O02755 PRELIMINARY; PRT; 348 AA.
 AC O02755;
 DT 01-JUL-1997 (TREMBREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBREL. 04, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBREL. 05, LAST ANNOTATION UPDATE)
 DE CCAAT/ENHANCER-BINDING BETA PROTEIN.
 GN C/EBP BETA.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN-JAPANESE BLACK CATTLE;
 RX MEDLINE; 97203913.
 RA YAMAOKA I., TANIGUCHI Y., SASAKI Y.;
 RL J. ANIM. SCI. 75:587-587(1997).
 DR EMBL; D82985; D1020911;
 SQ SEQUENCE 348 AA; 36390 MW; 76720BD9 CRC32;

Query Match 4.6%; Score 106; DB 6; Length 348;
 Best Local Similarity 23.3%; Pred. No. 2.64e-01;
 Matches 28; Conservative 35; Mismatches 49; Indels 8; Gaps 8;

Db 74 DFSPLYELGAPAPAPTASD-TFEAAPSAPAPVASSGQHDFLSDLFSDDYGGKNCK 132
 QY 7 DYGYLRS-SEEMSGVPGHPGLHPAPAPAPPPAASRSMFLA-LLGLGLGVVCS 64
 Db 133 KAAGYGVSLRGLGAALKHPG-CFAP-LHPPPPPPPPPAELKAEPPGEPADCKRKEA 190
 QY 65 IAL-FLYFR-AQMPDNRISEDSSTHCFYRLRLHENAGLQDSTLESDTL-PDCSRMKQA 121

Search completed: Fri Nov 13 17:18:57 1998

Job time : 131 secs.

W P S R L H (TW)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on on: Fri Nov 13 17:10:41 1998; MasPar time 9.91 Seconds
ular output not generated. 515.747 Million cell updates/sec

Title: >US-08-989-362-2
Description: (1-316) from US08989362.pep
Perfect Score: 2294
Sequence: 1 MRRASRDYKYLRSSEMGs.....LLDPDDATYFGAFKVQDID 316

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 33.982; Variance 147.062; scale 0.231

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	326	14.2	281	27	Human Apoptosis induc	5.41e-19
2	326	14.2	281	29	Human AGP-1.	5.41e-19
3	326	14.2	281	23	Novel cytokine Apo-2	5.41e-19
4	326	14.2	281	23	Human apoptosis induc	5.41e-19
5	282	12.3	291	29	Murine AGP-1.	5.30e-15
6	282	12.3	291	23	Mouse apoptosis induc	5.30e-15
7	176	7.7	182	23	CD40 ligand/zipper do	9.75e-06
8	174	7.6	137	14	Rat Fas ligand (part1	1.43e-05
9	174	7.6	138	15	Rat Fas ligand (part1	1.43e-05
10	174	7.6	178	14	C-terminally deleted	1.43e-05
11	175	7.6	179	23	Fas ligand.	1.18e-05
12	175	7.6	179	14	Human Fas ligand (par	1.18e-05
13	174	7.6	179	14	Rat Fas ligand (part1	1.43e-05
14	174	7.6	278	14	Rat Fas ligand encode	1.43e-05
15	175	7.6	281	26	Human Fas ligand.	1.18e-05
16	175	7.6	281	14	Human Fas-L protein.	1.18e-05
17	175	7.6	281	14	Human Fas ligand.	1.18e-05
18	175	7.6	281	19	Human Fas ligand deri	1.18e-05

19	174	7.6	281	18	R88356	Human Fas ligand.	1.43e-05
20	175	7.6	287	26	W27146	CH3/Fas ligand domain	1.18e-05
21	172	7.5	137	14	R79067	Mouse Fas ligand (par	2.11e-05
22	172	7.5	138	14	R79068	Mouse Fas ligand (par	2.11e-05
23	172	7.5	179	14	R79069	Mouse Fas ligand (par	2.11e-05
24	172	7.5	279	14	R79098	Mouse Fas ligand.	2.11e-05
25	170	7.4	279	18	R88357	Mouse Fas ligand.	3.10e-05
26	170	7.4	279	14	R77282	Mouse Fas-L protein.	3.10e-05
27	169	7.4	294	23	W03120	CD40 ligand/zipper do	3.75e-05
28	168	7.3	130	15	R79096	Human Fas ligand C-te	4.54e-05
29	168	7.3	136	14	R88307	N-terminally deleted	4.54e-05
30	168	7.3	137	14	R88306	N-terminally deleted	4.54e-05
31	168	7.3	137	14	R79100	Human Fas ligand (par	4.54e-05
32	168	7.3	138	14	R8305	N-terminally deleted	4.54e-05
33	168	7.3	138	15	R79064	Human Fas ligand (par	4.54e-05
34	168	7.3	139	14	R88304	N-terminally deleted	4.54e-05
35	168	7.3	141	14	R88303	N-terminally deleted	4.54e-05
36	168	7.3	151	26	W16667	Human Fas ligand (hFa	4.54e-05
37	167	7.3	180	23	W10875	FasL/IT-alpha hybrid.	5.50e-05
38	166	7.2	182	23	W24009	CD40 ligand/zipper do	6.66e-05
39	166	7.2	182	23	W24013	CD40 ligand/zipper do	6.66e-05
40	166	7.2	226	9	R49548	Predicted sequence en	6.66e-05
41	166	7.2	261	23	W09113	Human CD40L mutein C1	6.66e-05
42	165	7.2	261	11	R57469	CD40 ligand.	8.06e-05
43	165	7.2	261	10	R53969	Human CD40-L type II	8.06e-05
44	166	7.2	294	23	W09129	CD40 ligand/zipper do	6.66e-05
45	166	7.2	378	27	W35864	Human FAS-ligand:lgG2	6.66e-05

ALIGNMENTS

RESULT 1

ID W27134 standard; Protein; 281 AA.
AC W27134;
DT 02-APR-1998 (first entry)
DE Human Apoptosis inducing molecule-I (AIM-I).
KW Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
KW tumour necrosis factor ligand superfamily; AIM-I altered expression;
KW neoplasia inhibition; anti-inflammatory agent.
OS Homo sapiens.
PN W09733899-A1.
PD 18-SEP-1997.
PF 14-MAR-1996; U03773.
PR 14-MAR-1996; WO-U03773.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM;
DR WPI; 97-470807/43.
DR N-PSDB; T85210.
PT New isolated apoptosis inducing molecule-I - used to develop
PT products for the diagnosis and therapy of e.g. autoimmune diseases,
PT tumours, graft versus host disease or inflammation.
PS Claim 2; Fig 1; 82pp; English.
CC The present sequence represents a human Apoptosis inducing molecule-I
CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand
CC superfamily. The products can be used in the diagnosis and treatment of
CC disorders related to under-expression, over-expression or altered
CC expression of AIM-I. AIM-I or agonists can be used for treating
CC autoimmune disorders including systemic lupus erythematosus,
CC immunoproliferative disease lymphadenopathy (IPL),
CC angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit
CC neoplasia such as tumour cell growth, to treat restenosis, to regulate
CC haematopoiesis in endothelial cell development, to stimulate peripheral
CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
CC used for treating cachexia, cerebral malaria, rheumatoid arthritis
CC or osteoporosis, for preventing graft-host rejection, and as
CC anti-inflammatory agents, for treating endotoxic shock or to prevent
CC activation of HIV.
SQ Sequence 281 AA;
Query Match 14.2%; Score 326; DB 27; Length 281;
Best Local Similarity 35.9%; Pred. No. 5.41e-19;
Matches 47; Conservative 33; Mismatches 49; Indels 2; Gaps 2;

DE	Novel cytokine Apo-2 ligand.
KW	Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer;
OS	therapy.
FH	Homo sapiens.
Key	
FT	Location/Qualifiers
FT	peptide
FT	1..281 "Claim 4"
FT	/note= "Claim 4"
FT	protein
FT	15..281
FT	/note= "Claim 3"
FT	protein
FT	41..281
FT	/note= "Claim 2"
FT	protein
FT	114..281
FT	/note= "Claim 1"
FT	region
FT	1..14
FT	/label= Cytoplasmic_region
FT	region
FT	15..40
FT	/label= Transmembrane_region
FT	region
FT	41..281
FT	/label= Extracellular_region
FT	modified_site
FT	109
FT	/label= Glycosylation
FT	/note= "putative N-linked glycosylation site"
PN	WO9725428-A1.
PD	17-JUL-1997.
PF	08-JAN-1997; UO0272.
PR	09-JAN-1996; US-584031.
PA	(GETH) GENENTECH INC.
PI	Ashkenazi AJ, Chuntharapai A, Kim KJ;
DR	WPL; 97-372867/34.
DR	N-PSDB; T72796.
PT	Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
PT	apoptosis for the treatment of breast and colon cancer
CS	Claim 4; Fig 1a; 72pp; English.
CC	A novel cytokine (w1977), designated Apo-2 ligand, induces
CC	mammalian cell apoptosis. It is belived to be a member of the
CC	tumour necrosis factor cytokine family. Its amino acid sequence
CC	was deduced from a cDNA clone (T72796) isolated from a human
CC	placental cDNA library. Apo-2 ligand polypeptides, esp. those
CC	corresponding to amino acids 114-281, 41-281, 15-281 or 1-281 of
CC	Apo-2 ligand, can be produced by culturing cells transformed or
CC	transfected with a vector contg. Apo-2 ligand nucleic acid. They
CC	can be used to induce apoptosis in mammals and to treat
CC	pathological conditions such as cancer (esp. breast or colon
CC	cancer) or to raise antibodies useful in diagnostic assays.
SQ	Sequence 281 AA;
Query Match 14.28; Score 326; DB 23; Length 281;	
Best Local Similarity 35.98; Pred. No. 5.41e-19;	
Matches 47; Conservative 33; Mismatches 49; Indels 2; Gaps 2;	
Db	151 inswssrsghsflsnlhrlngelvihekfyvlysqtyfrgeekentkndqmvqi 210 :: : : : : : :
Qy	183 LSSWHYDR-GWAKISNTLNGKLRVNDGFYLYLANICFRHHETSGSVTDYLQLMYYV 241 : : : : : : :
Db	211 ykyt-sypdpillmksarnscwsdaeyglysiygqgfelfkendrifsvtnhlidmd 269 : : : : : : : : :
Qy	242 VKTSIKIPSSHNLMMKGSTKNWSGNSEFHYYSINVGFGFKLRAGEEITSIQVNSPLLDPD 301 : : : : : : :
Db	270 heasffgaflv 280 : :
Qy	302 QDATYFGAFKV 312 : :
RESULT	4
ID	WI9787 standard; Protein; 281 AA.
AC	WI9787;
DT	24-SEP-1997 (first entry)
DE	Human apoptosis inducer cytokine TRAIL.
DD	Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
KW	cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
KW	thrombotic microangioplasty; therapy.
OS	Homo sapiens.
FH	Key
FT	Location/Qualifiers


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FT domain 1..18
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FT domain 19..38
FT /label= Transmembrane_domain
FT domain 39..281
FT /label= Extracellular_domain
FT /note= "contains a receptor-binding region"
FT modified_site 109..111
FT /note= "potential N-glycosylation site"
FT cleavage_site 89..90
FT /note= "potential KEX2 protease processing site"
FT cleavage_site 149..150
FT /note= "potential KEX2 protease processing site"
FT WO9701633-A1.
FT PD 16-JAN-1997. U10895.
FT PF 25-JUN-1996; US-496632.
FT PR 29-JUN-1995; US-496632.
FT PA 01-NOV-1995; US-548368.
FT (IMMUNEX ) IMMUNEX CORP.
FT Goodwin RG, Wiley SR;
FT WPI: 97-118715/11.
FT N-PSDB; T72847.
PT TRAIL, a novel cytokine, induces apoptosis in cancer and
PT virus-infected cells - useful for treating thrombotic
PT microangiopathy, cancer and viral infection and for use in assays
PS Claim 10; Page 43-44; 62pp; English.
CC Human tumour necrosis factor related apoptosis inducing ligand
CC (TRAIL) (W19787) is a novel cytokine that induces apoptosis of
CC certain target cells, including cancer cells and virally infected
CC cells. Its amino acid sequence was deduced from cDNA clone HuAIC
CC (T72848), deposited in vector pDC409 as ATCC 69849. Recombinant
CC TRAIL polypeptides (esp. soluble polypeptides) can be expressed
CC in host cells and used in the treatment of cancer (e.g. leukaemia,
CC lymphoma and melanoma) and viral infections, or to raise antibodies
CC that may be useful for treating thrombotic microangiopathies.
SQ Sequence 281 AA;

Query Match 14.2%; Score 326; DB 23; Length 281;
Best Local Similarity 35.9%; Pred. No. 5.41e-19;
Matches 47; Conservative 33; Mismatches 49; Indels 2; Gaps 2;

Db 151 inswssrgshflnhrngelvihekgylyysqtyfrfqaekentkndkqvqi 210
QY 183 LSSWYHDR-GWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGSVPTDYQLMVVY 241
Db 211 ykvt-sypdpillmksarnscwskdaeyglysiygggifelkndrifsvtnehlidmd 269
242 VKTISKIPSSHNLMKGGSTKNWGNSEFHFYSINVGFFKLKLRAGEISIQVSNPSLLDPD 301
270 heasffgafv 280
QY 302 QDATVFGAFVK 312

RESULT 5
ID W44353 standard; Protein; 291 AA.
AC W44353;
DT 28-MAY-1998 (first entry)
DE Murine AGP-1.
KW Murine; AGP-1; tumour necrosis factor-related protein; TNF;
KW inflammation; bone resorption; haematopoietic disease.
OS Mus sp.
PN WO9746686-A2.
PD 11-DEC-1997.
PF 06-JUN-1997; U09895.
PR 07-JUN-1996; US-660562.
PA (AMGEN-) AMGEN INC.
PI Danilenko DM, Johnson MJ, Simonet WS;
DR WPI: 98-042194/04.
DR N-PSDB; V15294.
PT Nucleic acid encoding AGP-1, a tumour necrosis factor-related
PT protein - useful for treating inflammation, bone resorption and
PT haematopoietic diseases

PS Claim 10; Page 48-49; 62pp; English.

PS Claim 7; Page 33-34; 54pp; English.
CC The present sequence represents murine AGP-1. AGP-1 is a tumour-necrosis
CC factor (TNF)-related protein, involved in inflammation, myelopoiesis
CC and bone resorption. It has the same nucleic acid and amino acid (aa)
CC sequences as the TNF-related apoptosis-inducing ligand (TRAIL) described
CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds
CC are used to treat inflammation (e.g. rheumatoid arthritis, systemic
CC lupus erythematosus, psoriasis, scleroderma, infection-related
CC inflammation) or bone resorption diseases (e.g. osteoporosis,
CC osteomyelitis, hypercalcaemia, Paget's disease). AGP-1 can be used to
CC treat haematopoietic diseases associated with reduction in the number
CC of bone marrow cells, particularly neutrophils and lymphocytes, e.g.
CC where caused by disease, injury or exposure to myelosuppressive agents.
CC Host cells, transformed with expression vectors containing AGP-1 DNA,
CC are used to produce recombinant AGP-1.
SQ Sequence 291 AA;

Query Match 12.3%; Score 282; DB 29; Length 291;
Best Local Similarity 35.6%; Pred. No. 5.30e-15;
Matches 48; Conservative 37; Mismatches 42; Indels 8; Gaps 5;

Db 155 ieswssrkghsflnhrngelvihekgylyysqtyfrfqaedaskmvsdkvrtk 214
QY 183 LSSWYHDR-GWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGSVPTDYQLMVVY 241
Db 215 qlvgylykvt-sypdpillmksarnscwskdaeyglysiygggifelkndrifsvtne 273
QY 236 QLMVYVVKTSIKIPSSHNLMKGGSTKNWGNSEFHFYSINVGFFKLKLRAGEISIQVSNP 295
Db 274 hmdldgeasffgaf 288
QY 296 SLLDPDQDATVFGAF 310

RESULT 6
ID W19788 standard; Protein; 291 AA.
AC W19788;
DT 24-SEP-1997 (first entry)
DE Mouse apoptosis inducer cytokine TRAIL.
KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
KW thrombotic microangiopathy; therapy.
OS Mus musculus.
FH Key Location/Qualifiers
FT domain 1..17
FT /label= Cytoplasmic_domain
FT domain 18..38
FT /label= Transmembrane_domain
FT domain 39..291
FT /label= Extracellular_domain
FT modified_site 52..54
FT /note= "potential N-glycosylation site"
FT cleavage_site 85..86
FT /note= "potential KEX2 protease processing site"
FT cleavage_site 135..136
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FT cleavage_site 162..163
FT /note= "potential KEX2 protease processing site"
FT WO9701633-A1.
FT PD 16-JAN-1997.
FT PF 25-JUN-1996; U10895.
FT PR 29-JUN-1995; US-496632.
FT PA 01-NOV-1995; US-548368.
FT (IMMUNEX ) IMMUNEX CORP.
FT Goodwin RG, Wiley SR;
FT WPI: 97-118715/11.
FT N-PSDB; T72848.
PT TRAIL, a novel cytokine, induces apoptosis in cancer and
PT virus-infected cells - useful for treating thrombotic
PT microangiopathy, cancer and viral infection and for use in assays
PS Claim 10; Page 48-49; 62pp; English.
```

Query Match	7.6%	Score 174;	DB 14;	Length 137;
Best Local Similarity	26.7%	Pred. No. 1.43e-05;		
Matches	36;	Conservative 38;	Mismatches 53;	Indels 8; Gaps 6;

Db	11	srspile-wedtygtalisgvkkgglvlineaglyfvyskvyfrsq-scnsqp---lsh	65
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QY	178	SHKVTLSWYHDRGWAKISNMTLSNGKLRVQNQDGFYLYANICFRHETSGSVPTDYQL	237
		: : : : : : : :	
Db	66	kvm-r-nfkyopgdvlmee-kklmcycttgqivahasylgavfaltvadhlyvniqsls	122
		: : : : : : : : :	
QY	238	MVYVVTSTSIKIPSHNLKGGSTKNSGNSFEHFYSINVGGFPLKLRAGEEISIQVSNP	297
		: : : : : : : : :	
Db	123	infesktffglykl	137
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QY	298	LDPDQDATYGAQKV	312
		: : :	

RESULT	9
ID	R79063 standard; Protein; 138 AA.
AC	R79063;
DE	21-FEB-1996 (first entry)
DE	Rat Fas ligand (partial sequence).
KW	Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW	Fas cell surface antigen; Fas-L; rat.

PN WO9513293-AL.
 PD 18-MAY-1995.
 PF 10-NOV-1994; J01899.
 PR 10-NOV-1993; JP-305975.
 PR 13-DEC-1993; JP-342526.
 PR 18-MAR-1994; JP-074344.
 PR 08-JUL-1994; JP-180955.
 PR 07-SEP-1994; JP-239363.
 PR 18-OCT-1994; JP-278378.
 PA (MOCH) MOCHIDA PHARM CO LTD.
 PA (OSAB-) OSAKA BIOSCIENCE INST.
 PI Nagata S, Nakamura N, Suda T, Takahashi T;
 DR WPI; 95-194031/25.
 DR N-PSDB; Q99492.
 PT Peptide which binds to Fas antigen, and antibody reactive with it
 PT for treatment and diagnosis of viral or auto-immune diseases
 PS Claim 6; Page 213-215; 300pp; Japanese.
 CC Fas ligands or active fragments able to induce apoptosis in cells
 CC which express the Fas cell surface antigen are claimed. The
 CC proteins are isolated from human, rat and mouse sources. The present
 CC sequence represents part of the rat Fas ligand.
 CC Sequence 138 AA;
 Query Match 7.6%; Score 174; DB 15; Length 138;
 Best Local Similarity 26.7%; Pred. No. 1.43e-05;
 Matches 36; Conservative 38; Mismatches 53; Indels 8; Gaps 6;
 Db 12 sruple-wedtytalisgvykkggvlvneaglyfyvskvyfgrg-scnsqp---lsh 66
 QY 178 SHKVTLSWYHRCGWAKISNNLTSLNGKLRVNDQGFYLYANICFRHHETSGSVPTDYQL 237
 Db 67 kvym-r-nfkygdvlvnee-kklnycttgqiwahssylgavfnltvadhlyvnlsqsl 123
 QY 238 MYYVYKTSIRKIPSSHNLMKGGSTRNWSGSEFHFYSINVGFFKLRAGEEISIQVSNPSL 297
 Db 124 infeesktffglvkl 138
 QY 298 LDPDQDQTYFGAFV 312
 RESULT 10
 ID R88308 standard; Protein; 178 AA.
 AC R88308;
 DT 28-FEB-1996 (first entry)
 DE C-terminally deleted human Fas ligand CD179.
 KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
 KW Fas cell surface antigen; human; Fas-L; CD179; truncated.
 KW Homo sapiens.
 OS WO9513293-AL.
 PI 18-NOV-1995.
 PR 10-NOV-1994; J01899.
 PR 10-NOV-1993; JP-305975.
 PR 13-DEC-1993; JP-342526.
 PR 18-MAR-1994; JP-074344.
 PR 08-JUL-1994; JP-180955.
 PR 07-SEP-1994; JP-239363.
 PR 18-OCT-1994; JP-278378.
 PA (MOCH) MOCHIDA PHARM CO LTD.
 PA (OSAB-) OSAKA BIOSCIENCE INST.
 PI Nagata S, Nakamura N, Suda T, Takahashi T;
 DR WPI; 95-194031/25.
 PT Peptide which binds to Fas antigen, and antibody reactive with it
 PT for treatment and diagnosis of viral or auto-immune diseases
 PS Example 21; Page 196-197; 300pp; Japanese.
 CC CD179 is a truncated human Fas ligand from which the Leu residue at
 CC the C-terminus (position 179) has been deleted. Fas ligands able to
 CC induce apoptosis in cells which express the Fas cell surface antigen
 CC are claimed.
 CC Sequence 178 AA;
 Query Match 7.6%; Score 174; DB 14; Length 178;
 Best Local Similarity 24.0%; Pred. No. 1.43e-05;
 Matches 44; Conservative 54; Mismatches 75; Indels 10; Gaps 8;
 Db 15 lqkelaelr-estsqmhtassle-kqighpspppekelrkvahlgtgksnsrsmplew 62
 QY 130 LQHVIGPQRFSGAPAMMEGSLDVAQRGPEAQPFALHTINAASIPSGSHKVTLS-SWYH 188
 Db 63 tygivilsgvykkggvlvneaglyfyvskvyfgrg-scnnlp---lshkvym-rns-ky 116
 QY 189 DRGWAKISNNLTSLNGKLRVNDQGFYLYANICFRHHETSGSVPTDYQLQLMVYVVKTSIKI 248
 Db 117 pqdl-vmmegkmsycttgqmwarsylgavfnlttsadhllyvnvselslvnfeesqtf 175
 QY 249 PSSHNLMKGGSTRNWSGSEFHFYSINVGFFKLRAGEEISIQVSNPSLDDPDQDQTYFG 308
 Db 176 lyk 178
 QY 309 AFK 311
 RESULT 11
 ID W11814 standard; peptide; 179 AA.
 AC W11814;
 DT 20-OCT-1997 (first entry)
 DE Fas ligand.
 KW Human; Fas ligand; antigen; neutral; antibody; apoptosis; HIV;
 KW induction; assay; enzyme linked immunosorbant assay; diagnosis;
 KW disease; hepatitis B; hepatitis C; human immunodeficiency virus;
 KW graft versus host disease; ulcerative colitis; sequelae;
 KW myocardial infarction; treatment.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT peptide 24..43 /label= M52
 FT peptide 47..60 /label= M53
 FT peptide 60..72 /label= M54
 FT peptide 79..89 /label= M55
 FT peptide 89..107 /label= M56
 FT peptide 92..125 /label= M57
 FT peptide 126..141 /label= M58
 FT peptide 164..174 /label= M59
 PN WO9702290-AL.
 PD 23-JAN-1997.
 PF 01-JUL-1996; J01320.
 PR 17-MAY-1996; US-649100.
 PR 30-JUN-1995; JP-188480.
 PA (MOCH) MOCHIDA PHARM CO LTD.
 PA (OSAB-) OSAKA BIOSCIENCE INST.
 PI CO MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;
 DR WPI; 97-108917/10.
 PT Antibody reactive with Fas ligand capable of inducing apoptosis -
 PT used for diagnostic assay of Fas ligand in body fluids and for
 PT treatment of diseases in which Fas ligand/Fas antigen is involved
 PS Disclosure; Fig 1; 164pp; Japanese.
 CC Antigens derived from the present human Fas ligand sequence can
 CC be used in the preparation of a neutral antibody against an
 CC apoptosis inducing Fas ligand. The antibody can be used in a Fas
 CC ligand assay, e.g. an enzyme linked immunosorbant assay, to
 CC diagnose diseases in which the Fas ligand/Fas antigen system is
 CC implicated, e.g. hepatitis B/C, human immunodeficiency virus,
 CC graft/host disorders, ulcerative colitis or sequelae of myocardial
 CC infarction. The antibody may also be used to treat such diseases.
 CC Sequence 179 AA;
 Query Match 7.6%; Score 175; DB 23; Length 179;
 Best Local Similarity 23.9%; Pred. No. 1.18e-05;
 Matches 44; Conservative 55; Mismatches 75; Indels 10; Gaps 8;

Blue

DE	Rat Fas ligand (partial sequence).
KW	Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW	Fas cell surface antigen; Fas-L; rat.
OS	Rattus rattus.
PN	W09513293-Al.
PD	18-MAY-1995.
PR	10-NOV-1994; J01899.
PR	10-NOV-1993; JP-305975.
PR	13-DEC-1993; JP-342526.
PR	18-MAR-1994; JP-074344.
PR	08-JUL-1994; JP-180955.
PR	07-SEP-1994; JP-239363.
PR	18-OCT-1994; JP-278378.
PA	(MOCH) MOCHIDA PHARM CO LTD.
PA	(OSAB) OSAKA BIOSCIENCE INST.
PI	Nagata S, Nakamura N, Suda T, Takahashi T;
PI	WPI: 95-194031/25.
DR	N-PSDB; Q99495.
DR	Peptide which binds to Fas antigen, and antibody reactive with it
PT	for treatment and diagnosis of viral or auto-immune diseases
PS	Claim 7; Page 215-216; 300pp. Japanese.
CC	Fas ligands or active fragments able to induce apoptosis in cells
CC	which express the Fas cell surface antigen are claimed. The
CC	proteins are isolated from human, rat and mouse sources. The pres
CC	sequence represents part of the rat Fas ligand.
SC	Sequence 179 AA:
SO	

DR N-PSDB; Q93495; 20.
PT peptide which binds to Fas antigen, and antibody reactive with it -
PS for treatment and diagnosis of viral or auto-immune diseases
CC Claim 7; Page 215-216; 300pp; Japanese.
CC Fas ligands or active fragments able to induce apoptosis in cells
CC which express the Fas cell surface antigen are claimed. The
CC proteins are isolated from human, rat and mouse sources. The present
CC sequence represents part of the rat Fas ligand.
SQ Sequence 179 AA; 19

RESULT	14
ID	R79095 standard; Protein; 278 AA.
AC	R79095;
DE	20-FEB-1996 (first entry)
DT	Rat Fas ligand encoded by cDNA clone pTN24-15.
DW	Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW	Fas cell surface antigen; rat; fas-L.
KX	Rattus rattus.
OS	
FT	Key Location/Qualifiers
FE	77..99
FT	/label= transmembrane_anchor
FT	116
FT	/modified_site
FT	/label= N-glycosylation_site
FT	130
FT	/modified_site
FT	/label= N-glycosylation_site
FT	247
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FT	/label= N-glycosylation_site
FT	257
FT	/modified_site
FT	/label= N-glycosylation_site
PB	WO9513293-A1.
PN	

PK 18-MAR-1994; JP-074344.
 PR 08-JUL-1994; JP-180955.
 PR 07-SEP-1994; JP-239363.
 PR 18-OCT-1994; JP-278378.
 PA (MOCH) MOCHIDA PHARM CO LTD.

```

107 lqkelaelr-estsqmntassle-kqigpnsppbekkelrkvahltgknsrsmplewed 164
   | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
130 LOHVIGPQRFSGAPAMMEGSLWDVQGRPEAQPFPAHLTINAAISIPSGSHKVTLs-SWfH 188
   | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
165 tygavllsgvyk'kkgvlvlnetglyfvyakvyfrqg-scnnlp---lshkvym-rns-ky 218
   | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
189 DRGWAKISNNLTSLNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQMLWVYVKTsIKI 248
   | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
219 pqdl-vmmegkmnsycttgqmwarsylgavfnltadhlhlynnvselslvnfeesqtffg 277
   | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
249 PSSHNLKMGSTKNWSGNSEFHEFYsINVGFFKLRAGEETsIQVNSPSLDDPDQDAtYEG 308
   | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
278 lykI 281
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309 AFKV 312
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Search completed: Fri Nov 13 17:13:30 1998
Job time : 169 secs.

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MMRELF (TM)

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
on: Sat Nov 14 02:08:59 1998; MasPar time 2437.70 Seconds
1379.049 Million cell updates/sec
Abular output not generated.

Title: >US-08-989-362-1
Description: (1-2191) from US08989362.seq
Perfect Score: 2191
N.A. Sequence: 1 GCCAGGACCTCTGTGAACCG.....TTTGTGCTACTTAAATGGC 2191
Comp: CGCTCCTGGAGACACTTGGC.....AAACCATGAATTTTACCG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1988617 seqs, 767163441 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-est55
1:em_est10 2:em_est11

Database: genbank-est107
3:gb_est1 4:gb_est10 5:gb_est11 6:gb_est12 7:gb_est13
8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17
12:gb_est18 13:gb_est19 14:gb_est20 15:gb_est21
16:gb_est22 17:gb_est23 18:gb_est24 19:gb_est25
20:gb_est26 21:gb_est27 22:gb_est28 23:gb_est29 24:gb_est30
25:gb_est31 26:gb_est32 27:gb_est33 28:gb_est34 29:gb_est35

Statistics: Mean 12.352; Variance 2.924; scale 4.224

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	518	23.6	530	26	AA170348 ms88g11.r1 Soares mous	0.00e+00
2	133	6.1	419	8	AA504450 aa59h12.r1 NCI_CGAP_GC	7.17e-164
3	132	6.0	375	8	AA504211 aa59h12.s1 NCI_CGAP_GC	3.33e-162
4	64	2.9	252	13	AA754459 97SN1787 Rice Immature	1.73e-53
5	54	2.5	247	13	AA754458 97SN1784 Rice Immature	6.74e-39
6	55	2.5	252	13	AA754459 97SN1787 Rice Immature	2.51e-40
7	55	2.5	2275	11	AA754459 Homo sapiens ntcon2 co	2.51e-40
8	47	2.1	2275	11	AF034173 Homo sapiens ntcon2 co	4.02e-29
9	40	1.8	247	13	AA754458 97SN1784 Rice Immature	7.75e-20
10	30	1.4	282	9	AA573470 nm53f09.s1 NCI_CGAP_Br	8.08e-08
11	31	1.4	707	27	B19588 22203-T7.1 TAMU Arabid	6.20e-09
12	28	1.3	189	27	AQ068616 HS.2249.AL.H12.MF CIT	1.16e-05
13	29	1.3	407	27	AQ022111 CIT-HSP-230303.TR CIT-	9.96e-07

14	29	1.3	419	27	AQ046443	RPC111-34J1.TK RPOC11	9.96e-07
15	28	1.3	488	18	AI041106	CV61f03.x1 Soares_test	1.16e-05
16	29	1.3	623	27	AQ000570	CIT-HSP-228007.TF CIT-	9.96e-07
17	28	1.3	660	11	AF034177	Homo sapiens ntcon6 co	1.16e-05
18	28	1.3	719	27	B21675	F17P15-Sp6 IGF Arabido	1.16e-05
19	26	1.2	84	19	AA966799	s9d02al.r1 Aspergillus	1.29e-03
20	26	1.2	182	16	C89935	Dictyostellium discoide	1.29e-03
21	27	1.2	254	26	AA204255	mu26g12.r1 Soares 2NDM	1.29e-04
22	26	1.2	273	18	AA257887	EST 372 Boophilus micr	1.29e-03
23	26	1.2	280	16	AA832369	oc92b09.s1 NCI_CGAP_GC	1.29e-03
24	26	1.2	294	25	AA077530	7B44H12 Chromosome 7 F	1.29e-03
25	26	1.2	300	7	AA527345	ng40a02.s1 NCI_CGAP Co	1.29e-03
26	26	1.2	312	8	AA550088	118m3 gmbfHB3.1, G.	1.29e-03
27	26	1.2	337	6	CELK133GGR	C.elegans cdna clone y	1.29e-04
28	27	1.2	339	7	C23862	Dictyostellium discoide	1.29e-03
29	26	1.2	355	24	N98120	2212C3 czappFD2.1, De	1.29e-03
30	26	1.2	363	26	AA230383	mv73a12.r1 Soares mous	1.29e-03
31	26	1.2	402	17	AA938196	oc10e12.s1 NCI_CGAP_GC	1.29e-03
32	27	1.2	414	26	AA255819	zr84g08.r1 Soares NHHM	1.29e-04
33	26	1.2	439	11	AA701979	zi68d12.s1 Soares feta	1.29e-03
34	27	1.2	460	23	AA004088	mg80c11.r1 Soares mous	1.29e-04
35	26	1.2	460	13	AA776640	ae78g07.s1 Stratagene	1.29e-03
36	26	1.2	463	10	AA425966	zw17a06.r1 Soares ovar	1.29e-03
37	27	1.2	513	19	AA948367	cq46e12.s1 NCI_CGAP_K1	1.29e-04
38	26	1.2	514	8	AA279926	zs92g01.r1 NCI_CGAP_GC	1.29e-03
39	26	1.2	515	8	AA291434	zt44h08.r1 Soares ovar	1.29e-03
40	26	1.2	550	22	N98261	za28f09.r1 Homo sapien	1.29e-03
41	26	1.2	579	10	AA428848	zv50h12.r1 Soares ovar	1.29e-03
42	26	1.2	581	25	N58217	yv66h06.s1 Soares feta	1.29e-03
43	26	1.2	586	5	AA433286	EST100 prosophila mela	1.29e-03
44	26	1.2	696	16	C91060	Dictyostellium discoide	1.29e-03
45	27	1.2	866	17	C90750	Dictyostellium discoide	1.26e-04

ALIGNMENTS

RESULT LOCUS	AA170348	530 bp	msRNA	EST	16-FEB-1997
DEFINITION	ms88g11.r1 Soares mouse 3NbMS	Mus musculus	cdna clone	618692 5',	
ACCESSION	AA170348				
NID	91748900				
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 530)				
AUTHORS	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Weising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.				
TITLE	The WashU-HMI Mouse EST Project				
JOURNAL	Unpublished (1996)				
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.lbnl.gov) for further information. MGI:379516 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 490. Location/Qualifiers 1. 530 /organism="Mus musculus" /strain="C57BL/6J"				

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGCGCGCTGTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M. Fatima Bonaldo."
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/clone="618692"
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BASE COUNT
ORIGIN

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Best Local Similarity 99.2%; Pred. No. 0.00e+00;
Matches 527; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Db 1 AATGTTTCTGTGCAAGCTTTTGTAAATATATATTTGCTATAGTATTTGATTCAAAATA 60
QY 1588 AATGTTTCTGTGCAAGCTTTTGTAAATATATATTTGCTATAGTATTTGATTCAAAATA 1647
Db 61 TTTAAATGTCCTACTGTCACATATTAATGTTTAAATTTACAGATGATTTAACTG 120
QY 1648 TTTAAATGTCCTACTGTCACATATTAATGTTTAAATTTACAGATGATTTAACTG 1707
Db 121 GTGCACATTTGTAATCCCTGAGTACTGCTAGTATAGGGGCGAGACTGTTTCTGG 180
QY 1708 GTGCACATTTGTAATCCCTGAGTACTGCTAGTATAGGGGCGAGACTGTTTCTGG 1767
Db 181 TGACCACATGATGTTTATTTCTTTTAACTTAATAGAGCTCTCAGACTGTGCA 240
QY 1768 TGACCACATGATGTTTATTTCTTTTAACTTAATAGAGCTCTCAGACTGTGCA 1827
Db 241 AAACATGCAAGCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 300
QY 1828 AAACATGCAAGCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1887
Db 301 ATGTTGTCACACAGTGCCTTCAATTTAGAGCTAATTTAGAGCTGACATAG 360
QY 1888 ATGTTGTCACACAGTGCCTTCAATTTAGAGCTAATTTAGAGCTGACATAG 1947
Db 361 CCAAAAGGATACATAATAGGCTACTGAAA-TCTGTCAGGAGTATTTATGCAATTATTGA 419
QY 1948 CCAAAAGGATACATAATAGGCTACTGAAA-TCTGTCAGGAGTATTTATGCAATTATTGA 2007
Db 420 ACAGTGTCCTTTTTTACAAGAGCTACAAATGTAATTTTCTTTTTCCTCCATA 479
QY 2008 ACAGTGTCCTTTTTTACAAGAGCTACAAATGTAATTTTCTTTTTCCTCCATA 2067
Db 480 GAAATGATCTATAGTTTATCAGCCAAACAAATCCACTTTTTTAATTTAG 530
QY 2068 GAAATGATCTATAGTTTATCAGCCAAACAAATCCACTTTTTTAATTTAG 2118

RESULT 2
LOCUS AA504450 419 bp mRNA EST 18-AUG-1997
DEFINITION aa59h12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825287 5',
mRNA sequence.
ACCESSION AA504450
NID 92240610
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;

HOMO.
1 (Bases 1 to 419)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 400.
FEATURES
source
1..419
/organism="Homo sapiens"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGCGCGCTGTTTTTTTTTTTTTT-
3']. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="IMAGE:825287"
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BASE COUNT
ORIGIN

Query Match 6.1%; Score 133; DB 8; Length 419;
Best Local Similarity 83.3%; Pred. No. 7.17e-164;
Matches 204; Conservative 0; Mismatches 35; Indels 6; Gaps 5;
Db 181 CCTGGTCATGTGCCCTTCGCAGCT-GAAGTGGAGAGGCTGTCATCT-AGCGCAATTGA 238
QY 1395 CCTGGACATGTGCCCATGGAACCTTGAATTAAGAAGATGCCATGTCATTGCAAGAA 1454
Db 239 AGATCATCTGAAGGGCAAAATCTTTGAAATTTACATCATGCTGGACCTGCAAAA 298
QY 1455 ATGATAGTGTGAAGGGTAAAGTCTTTTGAATTTGATCATGCTGGACCTGCAAAA 1514
Db 299 A-TACTTTTT--CTAATGAGGAGAGAAA-TATATGTTATTTTATATAATCTAAAGTT 354
QY 1515 AGTCTTTTTTCTAATGAGGAGAGAAAATATATGTTATTTATATATGTCCTAAAGTT 1574
Db 355 ATATTTTCAGATGTAATGTTTTCTTTCGAAAGTATTTAAATATATTTGCTCTAGTAT 414
QY 1575 ATATTTTCAGTGAATGTTTTCTGTCGAAAGTTTTTCTGAAATTTATTTTGTGCTAGTAT 1634
Db 415 TTGAT 419
QY 1635 TTGAT 1639
RESULT 3

Db	211	TCAACAATTATATAACTACTCTGTGACAGATT--CAGTGGCCCCATTATGATCCTTTTTGG	269
Cp	2007	TCAATAATTGCATAAATACTCCTGACAGATTTTCAGTAGCCTATTATGATCCTTTTTGG	1948
Db	270	CAATGTCAGCTTTCAAAGTCAAATTAGTTCTCAAATTTTGAAGGCACCTGGTGGCCACA	329
Cp	1947	CTATGTCAGCTC-CTAAGTCAATTAGCTTCTCAAATTTTGAAGGCACCTGGTGGCCACA	1889
Db	330	TCCTGCTATTATTCAAGGCATCCATTTTAAATTTTTT	367
Cp	1888	TCCTACTATTATTCAAGATATTCATTTTATTTTATT	1851

RESULT	4	AA754459	252 bp	mRNA	EST	20-JAN-1998
LOCUS		97SN1787				
DEFINITION		Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.				

Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
REFERENCE
1 (bases 1 to 252)

TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL Unpublished (1998)

Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA

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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungido, Korea
Tel.: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahe@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.

```

FEATURES
  Location/Qualifiers
    seq
      primer: M13 REVERSE PRIMER.
      source
        1..252

```

```

i: 1202
/organism="Oryza sativa"
/cultivar="Milyang23"
/note="vector: pluscript SK(+); site_1: EcoRI; Site_2:
xhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1787"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"

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Query Match	2.9%;	Score 64;	DB 13;	Length 252;
Best Local	Similarity 10.7%;			
Matches	24;	Conservative	117;	Mismatches 82;
				Indels 2;
				Gaps 2;

Db 23 YBCHGNBVVVCVASHGNYSVHNCTBRGTHCDCKNVNWSTMTWGT VNWBNVSGDWHYWBV 82

Cp 839 CCATCAGCTGAAGATAGTCTGTAGGTACCGCTCCCGATGTTTCATGTATGCCGAAGCAAA 780

[illegible]

```
DB 83 BN1KVUVGNHTRCSRWRBVTIRMAHYHDYTNCSBYNNNDYHMWHBMYBBTGCMTCIMWCW 142
```

Cp 779 TGTGGCGTACAGGTAATAGAGCCATCTTGTTAACCT-TAGTTTCCGTTGCTAAC 721

Db 143 BHyNTKCTASGWHSTSYNDVKSSNTWGVTSYDKSMHGYCWBVKYHTKVSTRATRS 202

cp 720 GTCATGTTAGAGATCTTGGCCAGCCTCGATCGTGGTACCAAGAGGACA-GAGTGACTTT 662

RESULT 6

7	RESULT
	LOCUS
	DEFINITION
	ACCESSION
	NID
	KEYWORDS
	SOURCE
	ORGANISM

[illegible]

AF034173	2275 bp	mrna	EST	22-DEC-1997
Homo sapiens ntcon2	contig	mrna	partial sequence,	mrna sequence.
AF034173				
92707735				
EST.				
human.				
Homo sapiens				

2022

```

Query Match      1.8%; Score 40; DB 13; Length 247;
Best Local Similarity 10.1%; Pred. No. 7.75e-20;
Matches 17; Conservative 89; Mismatches 60; Indels 3; Gaps 3;

Db 69 YYARSKYGYGTBYXSNVYDNTGTGTGKTVNVHSGWNNRCSNVVYVWBTAYCDYBHY 128
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 2 CCAGGACCTCTGTGAACCGTGGCGGGCGGCCCTGGCGGAGTCTGCTCGCGCGT 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 129 BDRANHVDDTCTNDNRGVCNTASDNGTSATKRVYGYDKTSDCGGCKRWKVYTGSSBYB 188
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 GGGTGGCGGAGGAGAGACCA-TCGCGGA-TCGAGGCGGCCGGAACCTCGGCGGCC 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 189 RCGVNVVTRTTSMTDKSTKBSMDMSRRSVHYGRWBNKRGMSRW 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 CGGC-CATGCGCGCGGCGGAGACGACGCAAGTACGCGAGCTGCGGAGCT 167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
LOCUS AA573470 282 bp mRNA EST 12-SEP-1997
DEFINITION nm53f09.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1071977, mRNA
sequence.
ACCESSION AA573470
NID 92347998
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 282)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 328 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 99.
Location/Qualifiers
FEATURES
source
1..282
/organism="Homo sapiens"
/notes="vector: p7T3b-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified p7T3
vector. This library is the normalized version of
NCI_CGAP_Br1.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="IMAGE:1071977"
/clone_lib="NCI_CGAP_Br2"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
<1..>282
BASE COUNT 79 a 55 c 49 g 99 t
ORIGIN
Query Match 1.4%; Score 30; DB 9; Length 282;

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Best Local Similarity 75.0%; Pred. No. 8.08e-08;
Matches 45; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 4 TTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGACAGTGAGAAAGCTTTATTAA 63
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 1863 TTTTATTTTTTTTTTTTTTTGCTTGTCATAGTTTGTGACAGTCTGAAGACTCTATTAA 1804

RESULT 11
LOCUS B19588 707 bp DNA GSS 15-SEP-1997
DEFINITION T2203-T7.1 TAMU Arabidopsis thaliana genomic clone T2203, genomic
survey sequence.
ACCESSION B19588
NID 92394642
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; vascular plants; seed plants; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 707)
AUTHORS Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
Ecker, J.
TITLE BAC End Sequences at ATGC
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: T2203-T7, T2203-Sp6.1, T2203-Sp6.2,
T2203-Sp6.3, T2203-T7.2
Contact: Ecker, J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 96
High quality sequence stop: 181.
Location/Qualifiers
FEATURES
source
1..707
/organism="Arabidopsis thaliana"
/strain="Columbia"
/notes="Vector: BelobACII; Site_1: HindIII; Site_2:
HindIII; Produced by Rod Wing"
/db_xref="taxon:3702"
/clone="T2203"
/clone_lib="TAMU"
/sex="hermaphrodite"
BASE COUNT 136 a 149 c 78 g 208 t 136 others
ORIGIN
Query Match 1.4%; Score 31; DB 27; Length 707;
Best Local Similarity 39.1%; Pred. No. 6.20e-09;
Matches 34; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Db 485 TTTTATTTTTTTTTTTATTTATTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNA 544
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 1863 TTTTATTTTTTTTTTTATTTATTTGCTTGTCATAGTTTGTGACAGTCTGAAGACTCTATTAA 1804

Db 545 NNNNAANNANNANNNAACAANNAC 571
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Cp 1803 GTTAAAGAAATAAAGAAATAAACTAC 1777

RESULT 12
LOCUS AQ068616 189 bp DNA GSS 03-AUG-1998
DEFINITION HS_2249_AL_H12_MF Clt Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate-2249 Col-23 Row-O, genomic survey
sequence.
ACCESSION AQ068616
NID 93383815
KEYWORDS GSS.

```

```

SOURCE
ORGANISM      human.
               Homo sapiens
               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
               Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 189)
AUTHORS      Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
               Traicoif,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
TITLE        Construction of a Characterized Clone Resource for Genomic
               Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
               Tagged Connectors
JOURNAL      Unpublished (1997)
COMMENT      Contact: Mahairas GG, Wallace JC, Hood L
               High Throughput Sequencing Center
               University of Washington
               401 Queen Anne Avenue North, Seattle, WA 98109, USA
               Tel: (206) 616-3618
               Fax: (206) 616-3887
               Email: jwallace@u.washington.edu
               Sequence Tagged Connector
               Plate: 2249 row: 0 column: 23
               Class: BAC ends
               High quality sequence stop: 189.
               Location/Qualifiers
               1..189
               /organism="Homo sapiens"
               /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
               E-Coli DH10B"
               /db_xref="taxon:9606"
               /clone="Plate=2249 Col=23 Row=0"
               /clone_lib="CIT Approved Human Genomic Sperm Library D"
               /sex="male"
BASE COUNT   40 a 48 c 30 g 59 t 2 others
ORIGIN
Query Match 1.3%; Score 28; DB 27; Length 189;
Best Local Similarity 96.7%; Pred. No. 1.16e-05;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 24 TATTCCTTTTATTTTATTTATTTATTTG 53
||||| ||||||| ||||||| ||||||| |||||||
Cp 1869 TATTCATTTTATTTTATTTATTTATTTG 1840

RESULT 13
LOCUS      AQ022111 407 bp DNA GSS 08-JUN-1998
DEFINITION CIT-HSP-2303D3.TR CIT-HSP Homo sapiens genomic clone 2303D3,
               genomic survey sequence.
CESSION   AQ022111
KEYWORDS  GSS.
SOURCE    human.
ORGANISM  Homo sapiens
               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
               Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 407)
AUTHORS    Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
               Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
               Simon,M. and Venter,J.C.
TITLE      Use of a random BAC End Sequence Database for Sequence-Ready Map
               Building
JOURNAL    Unpublished (1997)
COMMENT    Contact: Mark Adams
               Department of Eukaryotic Genomics
               The Institute for Genomic Research
               9712 Medical Center Dr., Rockville, MD 20850, USA
               Tel: 301 838 0200
               Fax: 301 838 0208
               Email: mdadams@tigr.org
               Clones are available from Research Genetics (info@resgen.com). BAC
               end search page:
               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

SOURCE
ORGANISM      human.
               Homo sapiens
               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
               Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 189)
AUTHORS      Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
               Traicoif,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
TITLE        Construction of a Characterized Clone Resource for Genomic
               Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
               Tagged Connectors
JOURNAL      Unpublished (1997)
COMMENT      Contact: Mahairas GG, Wallace JC, Hood L
               High Throughput Sequencing Center
               University of Washington
               401 Queen Anne Avenue North, Seattle, WA 98109, USA
               Tel: (206) 616-3618
               Fax: (206) 616-3887
               Email: jwallace@u.washington.edu
               Sequence Tagged Connector
               Plate: 2249 row: 0 column: 23
               Class: BAC ends
               High quality sequence stop: 189.
               Location/Qualifiers
               1..189
               /organism="Homo sapiens"
               /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
               E-Coli DH10B"
               /db_xref="taxon:9606"
               /clone="Plate=2249 Col=23 Row=0"
               /clone_lib="CIT Approved Human Genomic Sperm Library D"
               /sex="male"
BASE COUNT   40 a 48 c 30 g 59 t 2 others
ORIGIN
Query Match 1.3%; Score 28; DB 27; Length 189;
Best Local Similarity 96.7%; Pred. No. 1.16e-05;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 24 TATTCCTTTTATTTTATTTATTTATTTG 53
||||| ||||||| ||||||| ||||||| |||||||
Cp 1869 TATTCATTTTATTTTATTTATTTATTTG 1840

RESULT 13
LOCUS      AQ022111 407 bp DNA GSS 08-JUN-1998
DEFINITION CIT-HSP-2303D3.TR CIT-HSP Homo sapiens genomic clone 2303D3,
               genomic survey sequence.
CESSION   AQ022111
KEYWORDS  GSS.
SOURCE    human.
ORGANISM  Homo sapiens
               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
               Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 407)
AUTHORS    Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
               Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
               Simon,M. and Venter,J.C.
TITLE      Use of a random BAC End Sequence Database for Sequence-Ready Map
               Building
JOURNAL    Unpublished (1997)
COMMENT    Contact: Mark Adams
               Department of Eukaryotic Genomics
               The Institute for Genomic Research
               9712 Medical Center Dr., Rockville, MD 20850, USA
               Tel: 301 838 0200
               Fax: 301 838 0208
               Email: mdadams@tigr.org
               Clones are available from Research Genetics (info@resgen.com). BAC
               end search page:
               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1..407
/organism="Homo sapiens"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"
/db_xref="taxon:9606"
/clone="2303D3"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
BASE COUNT   135 a 60 c 72 g 140 t
ORIGIN
Query Match 1.3%; Score 29; DB 27; Length 407;
Best Local Similarity 77.4%; Pred. No. 9.96e-07;
Matches 48; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

Db 34 TCAGAGCTCTTTACATATTTTAAACAACTACTTTTACCACATATATGATTTGCTAGTACT 93
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Cp 1662 TGAGACATTTTAAATATTTT-GAATCAAAATCTATAGCACAAATATAATTACAAACT 1604

Db 94 TT 95
||
Cp 1603 TT 1602

RESULT 14
LOCUS      AQ046443 419 bp DNA GSS 13-JUL-1998
DEFINITION RPC111-34J1.TK RPC111 Homo sapiens genomic clone R-34J1, genomic
               survey sequence.
ACCESSION  AQ046443
NID        G3315370
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
               Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 419)
AUTHORS    Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
               Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
               Venter,J.C.
TITLE      Use of BAC End Sequences for Sequence-Ready Map Building
JOURNAL    Unpublished (1997)
COMMENT    Other GSSs: RPC111-34J1.TJ
               Contact: Mark Adams
               Department of Eukaryotic Genomics
               The Institute for Genomic Research
               9712 Medical Center Dr., Rockville, MD 20850, USA
               Tel: 301 838 0200
               Fax: 301 838 0208
               Email: mdadams@tigr.org
               For clone availability, please contact Pieter de Jong
               (pieter@jong.med.buffalo.edu). Clones may be purchased from
               Research Genetics (info@resgen.com). BAC end search page:
               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
               Class: BAC ends.
               Location/Qualifiers
               1..419
               /organism="Homo sapiens"
               /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
               RPC111 Human Male BAC Library"
               /db_xref="taxon:9606"
               /clone="R-34J1"
               /clone_lib="RPC111"
               /sex="Male"
               /cell_type="Lymphocytes"
BASE COUNT   131 a 73 c 76 g 139 t
ORIGIN
Query Match 1.3%; Score 29; DB 27; Length 419;
Best Local Similarity 77.4%; Pred. No. 9.96e-07;

```

Matches	48;	Conservative	0;	Mismatches	13;	Indels	1;	Gaps	1;
---------	-----	--------------	----	------------	-----	--------	----	------	----

Db 402 AG 403

RESULT	15				
LOCUS		AI041106	488 bp	mRNA	EST
DEFINITION		ov61f03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641821.3', mRNA sequence.			

NID g3280300

SOURCE human.

Eukaryotes
Primates

AUTHORS NCI-CGAP

Tumor Gen

COMMENT

TEL: (303) 440-1000
Email: info@hawaii.com

Bonaldo,

DNA Sequencing

found this

See primary

FEATURES

10

1

ORIGIN

Query Match

Matches 44; **Con**

4
4
4
4
4
4
0
0
4
4

7
7

9
9

Search completed: Sat Nov 14 03:12:39 1998

W P S R E H (TM)

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Distribution rights by Oxford Molecular Ltd

MPsrch_nrn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Nov 14 03:21:01 1998; Maspar time 84.28 Seconds
1212.676 Million cell updates/sec
Circular output not generated.

Title: >US-08-989-362-1
Description: (1-2191) from US08989362.seq
Perfect Score: 2191
N.A. Sequence: 1 GCCAGGACCTCTGTGACCG.....TTTGGTACTTAAATGGC 2191
Comp: CGGTCTGGACACATTGGC.....AAACCATGAATTTTACCG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 88822 seqs, 23323279 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 9.409; Variance 5.535; scale 1.700

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	47	2.1	7218	1	US-08-232- Sequence 14, Applicati	1.14e-13
2	41	1.9	7218	1	US-08-232- Sequence 14, Applicati	4.08e-10
3	39	1.8	215	1	US-08-238- Sequence 5, Applicati	5.86e-09
4	35	1.6	215	1	US-08-238- Sequence 5, Applicati	1.07e-06
5	26	1.2	85	2	PCT-US94-0 Sequence 26, Applicati	6.15e-02
6	26	1.2	85	2	PCT-US94-0 Sequence 1, Applicati	6.15e-02
7	26	1.2	85	1	US-08-438- Sequence 26, Applicati	6.15e-02
8	26	1.2	85	1	US-08-370- Sequence 26, Applicati	6.15e-02
9	27	1.2	105	1	US-07-865- Sequence 13, Applicati	1.95e-02
10	24	1.1	66	1	US-08-471- Sequence 144, Applicat	5.78e-01
11	24	1.1	69	1	US-08-471- Sequence 142, Applicat	5.78e-01
12	24	1.1	74	2	PCT-US95-1 Sequence 94, Applicati	5.78e-01
13	24	1.1	74	2	PCT-US95-1 Sequence 100, Applicat	5.78e-01
14	24	1.1	74	2	PCT-US95-1 Sequence 94, Applicati	5.78e-01
15	24	1.1	75	2	PCT-US95-1 Sequence 99, Applicati	5.78e-01
16	24	1.1	75	2	PCT-US95-1 Sequence 99, Applicati	5.78e-01
17	24	1.1	81	2	PCT-US95-1 Sequence 92, Applicati	5.78e-01
18	24	1.1	81	2	PCT-US95-1 Sequence 98, Applicati	5.78e-01
19	25	1.1	81	2	PCT-US95-1 Sequence 92, Applicati	1.91e-01
20	24	1.1	82	2	PCT-US95-1 Sequence 97, Applicati	5.78e-01

c	21	24	1.1	82	2	PCT-US95-1	Sequence 97, Applicati	5.78e-01
	22	24	1.1	4131	2	PCT-US92-0	Sequence 3, Applicati	5.78e-01
	23	25	1.1	7970	1	US-08-135-	Sequence 31, Applicati	1.91e-01
	24	23	1.0	65	1	US-08-471-	Sequence 145, Applicat	1.71e+00
c	25	22	1.0	66	1	US-08-471-	Sequence 144, Applicat	4.93e+00
	26	23	1.0	68	1	US-08-471-	Sequence 143, Applicat	1.71e+00
c	27	23	1.0	105	1	US-07-865-	Sequence 13, Applicati	1.71e+00
	28	22	1.0	1312	2	PCT-US94-0	Sequence 1, Applicati	4.93e+00
	29	22	1.0	1817	1	US-08-473-	Sequence 5, Applicati	4.93e+00
	30	22	1.0	2060	1	PCT-US91-0	Sequence 2, Applicati	4.93e+00
	31	22	1.0	2060	1	US-07-721-	Sequence 31, Applicati	1.71e+00
	32	23	1.0	2107	1	US-08-390-	Sequence 1, Applicati	1.71e+00
	33	23	1.0	2504	1	US-08-484-	Sequence 15, Applicati	1.71e+00
	34	23	1.0	2504	1	US-08-484-	Sequence 15, Applicati	1.71e+00
	35	23	1.0	2823	1	US-08-398-	Sequence 1, Applicati	1.71e+00
	36	22	1.0	3024	3	5284931-1	Patent No. 5284931.	4.93e+00
	37	23	1.0	3136	1	US-08-332-	Sequence 41, Applicati	1.71e+00
	38	23	1.0	3136	1	US-08-188-	Sequence 41, Applicati	1.71e+00
	39	22	1.0	3291	2	PCT-US94-0	Sequence 1, Applicati	4.93e+00
	40	23	1.0	3590	1	US-08-587-	Sequence 1, Applicati	4.93e+00
	41	23	1.0	3590	2	PCT-US96-0	Sequence 1, Applicati	4.93e+00
c	42	22	1.0	4032	1	US-08-107-	Sequence 3, Applicati	4.93e+00
c	43	22	1.0	4032	2	PCT-US92-0	Sequence 3, Applicati	4.93e+00
c	44	22	1.0	5852	1	US-07-867-	Sequence 2, Applicati	4.93e+00
	45	22	1.0	17327	1	US-07-906-	Sequence 15, Applicati	4.93e+00

ALIGNMENTS

RESULT 1
ID US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
AC xxxxxx
DT Sequence 14, Application US/08232463
CC Sequence 14, Application US/08232463
CC Patent No. 5670367
CC GENERAL INFORMATION:
CC APPLICANT: DORNER, F.
CC APPLICANT: SCHEIFLINGER, F.
CC APPLICANT: FALKNER, F. G.
CC TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CC NUMBER OF SEQUENCES: 52
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Foley & Lardner
CC STREET: 1800 Diagonal Road, Suite 500
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-0299
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/232,463
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/07/935,313
CC FILING DATE:
CC APPLICATION NUMBER: EP 91 114 300.6
CC FILING DATE: 26-AUG-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BENT, Stephen A.
CC REGISTRATION NUMBER: 29,768
CC REFERENCE/DOCKET NUMBER: 30472/114 IMMU
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (703)836-9300
CC TELEFAX: (703)683-4109
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:

```

CC LENGTH: 7218 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC IMMEDIATE SOURCE:
CC CLONE: pTZ9pt-F15
SQ SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.

Query Match      2.1%   Score 47;  DB 1;  Length 7218;
Best Local Similarity 7.9%;  Pred. No. 1.14e-13;
Matches 14;  Conservative 98;  Mismatches 65;  Indels 0;  Gaps 0;

Db      1045  GCAGGTCAGGAGCTGCATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1104
      |||| |||  |||| |  |  : : : : :  : : : : :  : : : : :  : : : : :
Qy      162  GCAGCTCGGAGAGATGGGACGGCCCGCTCCACACAGAGGTCGCTGCACCCG 221

Db      1105  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1164
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
Qy      222  CGCTTCTGCACCGGCTCGCGCGCGCACCCGCGGCTCCCGCTCCATGTTCTCGGCC 281

Db      1165  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1221
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
Qy      282  TCTGTGGCGCTGGACATGGCGAGCTGTCTGTCAGCATCGCTCTGTGCTCTACTTTC 338

```

RESULT 2
 ID US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
 AC AC
 DT xxxxxx
 DE
 Sequence 14, Application US/08232463
 Sequence 14, Application US/08232463
 Patent No. 5670367
 CC
 GENERAL INFORMATION:
 CC APPLICANT: DORNER, F.
 CC APPLICANT: SCHEIFLINGER, F.
 CC APPLICANT: FALKNER, F. G.
 CC TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 CC NUMBER OF SEQUENCES: 52
 CC
 CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Foley & Lardner
 CC STREET: 1800 Diagonal Road, Suite 500
 CC CITY: Alexandria
 CC STATE: VA
 CC COUNTRY: USA
 CC ZIP: 22313-0299
 CC
 COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC
 CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/232,463
 CC FILING DATE:
 CC CLASSIFICATION: 435
 CC
 PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/935,313
 CC FILING DATE:
 CC APPLICATION NUMBER: EP 91 114 300.6
 CC FILING DATE: 26-AUG-1991
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: BENT, Stephen A.
 CC
 REGISTRATION NUMBER: 29,768
 CC
 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 CC
 TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (703)836-9300
 CC TELEFAX: (703)683-4109
 CC TELEX: 899149
 CC
 INFORMATION FOR SEQ ID NO: 14:
 CC
 SEQUENCE CHARACTERISTICS:
 CC LENGTH: 7218 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear

```
CC IMMEDIATE SOURCE:  
CC CLONE: ptzgpt-FIs  
SQ SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.  
  
Query Match      1.9%; Score 41; DB 1; Length 7218;  
Best Local Similarity 0.5%; Pred. No. 4.08e-10;  
Matches       1; Conservative 113; Mismatches 73; Indels   0; Gaps    0  
  
Db     1249 YYYYYYYYYYYYYYYY : : : : : : : : : : : : : : : : : :  
          : : : : : : : : : : : : : : : : : : : : : : : :  
Cp     2012 CCTGTTCAATAATTCGCATAAATACTCTCGACAGATTCTTTCAGTAGCCGTATTATGTCCTT 1953  
        : : : : : : : : : : : : : : : : : : : : : : : :  
Db     1309 YYYYYYYYYYYYYYYY : : : : : : : : : : : : : : : : : :  
          : : : : : : : : : ~ : : : : : : : : : : : : : :  
Cp     1952 TTTCGGCATGTCACCTCCTAAAGTCAAATTAGCTTCTTAATTTGAAGCACCTGGTGACC 1893  
        : : : : : : : : : : : : : : : : : : : : : : : :  
Db     1369 YYYYYYYYYYYYYYYY : : : : : : : : : : : : : : : : : :  
          : : : : : : : : : : : : : : : : : : : : : : : :  
Cp     1992 AACATCCTACTTATATTCAGAATATTCATTTTTATTTTTATTTATTTGCTGCAT 1833  
        : : : : : : : : : : : : : : : : : : : : : : : :  
Db     1429 YYYYYYG 1435  
          : : : !  
Cc     1832 AGTTTGTG 1826
```

RESULT 3
 ID US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
 AC xxxxxx
 DT
 Sequence 5, Application US/08238163
 DE Sequence 5, Application US/08238163
 CC Patent No. 5569830
 CC GENERAL INFORMATION:
 CC APPLICANT: BENNETT, Alan
 CC APPLICANT: LABAVITCH, John M.
 CC APPLICANT: POWELL, Ann
 CC APPLICANT: STOTZ, Henrik
 CC TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
 CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
 CC NUMBER OF SEQUENCES: 24
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: Steuart Street Tower, One Market Plaza
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94105-1493
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/238,163
 CC FILING DATE: 03-MAY-1994
 CC CLASSIFICATION: 800
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Bastian, Kevin L.
 CC REGISTRATION NUMBER: 34,774
 CC REFERENCE/DOCKET NUMBER: 2307E-540
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 543-9600
 CC TELEFAX: (415) 543-5043
 CC INFORMATION FOR SEQ ID NO: 5:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 215 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: unknown
 CC MOLECULE TYPE: protein
 CC FEATURE:
 CC NAME/KEY: misc.feature
 CC LOCATION: 1..215

CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 66 bases
CC	TYPE: nucleic acid
CC	STRANDEDNESS: single
CC	TOPOLOGY: unknown
CC	MOLECULE TYPE: DNA
SQ	SEQUENCE 66 BP; 2 A; 3 C; 4 G; 2 T; 55 OTHER.
Query Match 1.8; Score 24; DB 1; Length 66;	
B	Best Local Similarity 9.8%; pred. No. 5.78e-01;
M	Matches 6; Conservative 18; Mismatches 37; Indels 0; Gaps 0;
D	b 2 CGAGNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNC 61
Q	y 202 CGAGGTCGCCTCACCCCGCCTTCTGTGACCGGGTCCGCCGCGCACCCGCGCTC 261
D	b 62 C 62
Q	y 262 C 262
RESULT 11	
A	C US-08-471-052A-142 STANDARD; DNA; UNC; 69 BP.
D	T xxxxxx
D	E Sequence 142, Application US/08471052A
DE	Sequence 142, Application US/08471052A
CC	Patent No. 5625033
CC	GENERAL INFORMATION:
CC	APPLICANT: Kay, B. K.
CC	APPLICANT: Fowkes, D. M.
CC	TITLE OF INVENTION: Totally Synthetic Affinity Reagents
CC	NUMBER OF SEQUENCES: 166
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Pennie & Edmonds
CC	STREET: 1155 Avenue of the Americas
CC	CITY: New York
CC	STATE: New York
CC	COUNTRY: U.S.A.
CC	ZIP: 10036-2711
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/471,052A
CC	FILING DATE: 06-JUNE-1995
CC	CLASSIFICATION: 530
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Misrock, S. Leslie
CC	REGISTRATION NUMBER: 18,872
CC	REFERENCE/DOCKET NUMBER: 1101-179
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: 212 790-9090
CC	TELEFAX: 212 869-8864/9741
CC	TELEX: 66141 PENNIE
CC	INFORMATION FOR SEQ ID NO: 142:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 69 bases
CC	TYPE: nucleic acid
CC	STRANDEDNESS: single
CC	TOPOLOGY: unknown
CC	MOLECULE TYPE: DNA
SQ	SEQUENCE 69 BP; 2 A; 4 C; 6 G; 2 T; 55 OTHER.
Query Match 1.8; Score 24; DB 1; Length 69;	
B	Best Local Similarity 9.8%; pred. No. 5.78e-01;
M	Matches 6; Conservative 18; Mismatches 37; Indels 0; Gaps 0;
D	b 5 CGAGNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNC 64
Q	y 202 CGAGGTCGCCTCACCCCGCCTTCTGTGACCGGGTCCGCCGCGCACCCGCGCTC 261

```

Db      65 C 65
      1
QY      262 C 262

RESULT 12
ID      PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
AC      xxxxxx
DT
DE      Sequence 94, Application PC/TUS9511934
CC      Sequence 94, Application PC/TUS9511934
CC      GENERAL INFORMATION:
CC      APPLICANT: CytoGen Corporation
CC      TITLE OF INVENTION: Antigen Binding Peptides (Aptides) From
CC      TITLE OF INVENTION: Peptide Libraries
CC      NUMBER OF SEQUENCES: 103
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Pennie & Edmonds
CC      STREET: 1155 Avenue of the Americas
CC      CITY: New York
CC      STATE: New York
CC      COUNTRY: USA
CC      ZIP: 10036
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: PCT/US95/11934
CC      FILING DATE: 20-SEP-1995
CC      CLASSIFICATION:
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Misrock, S. Leslie
CC      REGISTRATION NUMBER: 18,872
CC      REFERENCE/DOCKET NUMBER: 1101-196-228
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (212) 790-9090
CC      TELEFAX: (212) 869-9741/8664
CC      TELEX: 66141 PENNIE
CC      INFORMATION FOR SEQ ID NO: 94:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 74 base pairs
CC      TYPE: nucleic acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: DNA (genomic)
CC      SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
SQ

Query Match      1.18; Score 24; DB 2; Length 74;
Best Local Similarity 6.23; Pred. No. 5.78e-01;
Matches      4; Conservative 20; Mismatches 41; Indels 0; Gaps 0;

Db      2 CGAGNNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBN 61
      |||| : : : : : : : : : : : : : : : : : : : : : :
QY      202 CGAGGTCCGCTGCACCCCGCGCTTCGACCGGCTCGCGCGCCGCGCTC 261
      |||| : : : : : : : : : : : : : : : : : : : : : :
Db      62 BNNBN 66
      : :
QY      262 CCGCT 266

RESULT 13
ID      PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
AC      xxxxxx
DT
DE      Sequence 100, Application PC/TUS9511934
CC      Sequence 100, Application PC/TUS9511934
CC      GENERAL INFORMATION:
CC      APPLICANT: CytoGen Corporation
CC      TITLE OF INVENTION: Antigen Binding Peptides (Aptides) From
CC      TITLE OF INVENTION: Peptide Libraries

```

CC	NUMBER OF SEQUENCES:	103
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: Pennie & Edmonds	
CC	STREET: 1155 Avenue of the Americas	
CC	CITY: New York	
CC	STATE: New York	
CC	COUNTRY: USA	
CC	ZIP: 10036	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Floppy disk	
CC	COMPUTER: IBM PC compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: PCT/US95/11934	
CC	FILING DATE: 20-SEP-1995	
CC	CLASSIFICATION:	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: Misrock, S. Leslie	
CC	REGISTRATION NUMBER: 18,872	
CC	REFERENCE/DOCKET NUMBER: 1101-196-228	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: (212) 790-9090	
CC	TELEFAX: (212) 869-9741/8864	
CC	TELEX: 66141 PENNIE	
CC	INFORMATION FOR SEQ ID NO: 100:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 74 base pairs	
CC	TYPE: nucleic acid	
CC	STRANDEDNESS: single	
CC	TOPOLOGY: linear	
CC	MOLECULE TYPE: DNA (genomic)	
SQ	SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.	
	Query Match	1.18; Score 24; DB 2; Length 74;
	Best Local Similarity	10.38; Pred. No. 5.78e-01;
	Matches	7; Conservative 19; Mismatches 42; Indels 0; Gaps 0;
Db	3 AGAVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNN 62	
QY	81 AGACGATCGGGAGCAGGCGGCCGCGACTTCGGGGCCGCGCATGTGC	
	: :	
Db	63 VNNACCAC 70	
QY	141 GAGACTAC 148	
	:	
RESULT	14	
	PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.	
	xxxxxx	
DE	Sequence 94, Application PC/TUS9511934	
CC	Sequence 94, Application PC/TUS9511934	
CC	GENERAL INFORMATION:	
CC	APPLICANT: CytoGen Corporation	
CC	TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From	
CC	TITLE OF INVENTION: Peptide Libraries	
CC	NUMBER OF SEQUENCES: 103	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: Pennie & Edmonds	
CC	STREET: 1155 Avenue of the Americas	
CC	CITY: New York	
CC	STATE: New York	
CC	COUNTRY: USA	
CC	ZIP: 10036	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Floppy disk	
CC	COMPUTER: IBM PC compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: PCT/US95/11934	
CC	FILING DATE: 20-SEP-1995	

Search completed: Sat Nov 14 03:23:58 1998
Job time : 177 secs.

(TM)

Result	No.	Score	Query		Length	DB	ID	Description	Pred. No.
			Match						
1	43	2.0	91	9	Q51746	Oligonucleotide probe	5.16e-09		
c	41	1.9	204	1	N81164	Base substituted E.co	5.67e-08		
c	3	40	1.8	91	Q51746	Oligonucleotide probe	1.86e-07		
5	39	1.8	204	1	N81164	Base substituted E.co	6.03e-07		
5	37	1.7	178	32	T76405	Human endothelin-1 an	6.19e-06		
c	37	1.7	178	32	T76405	Human endothelin-1 an	6.19e-06		
c	35	1.6	88	32	T76170	Human IL3 receptor an	6.11e-05		
8	36	1.6	114	12	Q70469	Generic DNA sequence	1.96e-05		
9	36	1.6	114	12	Q70465	Generic DNA sequence	1.96e-05		
10	34	1.6	114	12	Q70457	Generic DNA sequence	1.89e-04		
11	34	1.6	114	12	Q70458	Generic DNA sequence	1.89e-04		
c	12	35	1.6	114	12	Q70467	Generic DNA sequence	6.11e-05	
c	13	35	1.6	114	12	Q70469	Generic DNA sequence	6.11e-05	

[illegible]

Synthetic.
W09640162-A1.
19-DEC-1996.
06-JUN-1996; U09306.
07-JUN-1995; US-474497.
(UYEC-) UNIV EAST CAROLINA.
Metzger WJ, Nyce JW;
WPI; 97-051871/05.
Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of subject
Claim 5; Page 38; 71pp; English.
A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the human endothelin-1, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-reactive airways.
Sequence 178 BP; 0 A; 52 C; 46 G; 32 T;
Query Match 1.7%; Score 37; DB 32; Length 178;
Best Local Similarity 35.3%; Pred. No. 6.19e-06;
Matches 36; Conservative 36; Mismatches 29; Indels 1; Gaps 1;
70 cbgagcctbbgctgc-tgtttctggbgctccttggbgcbcbcbcbgbbgbb 128
233 CGCCGCCCTCCGCTCCATGTTCTTCCTGGCTCGGGCTGGGACGAGTGGTCTG 312
129 btcbtgbcbbtbtccttcgtbbbbbgbggtcbbbbb 170
313 CAGCATCGCTCTGTTCCCTGACTTTCGACGCGAGATGCATCC 354
15-SEP-1997 (first entry)
Human endothelin-1 antisense oligonucleotide.
Asthma; airway epithelium; adenosine free; cystic fibrosis;
chronic obstructive pulmonary disease; bronchitis; ss.
Synthetic.
W09640162-A1.
19-DEC-1996.
06-JUN-1996; U09306.
07-JUN-1995; US-474497.
(UYEC-) UNIV EAST CAROLINA.
Metzger WJ, Nyce JW;
WPI; 97-051871/05.
Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of subject
Claim 5; Page 38; 71pp; English.
A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the human endothelin-1, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-reactive airways.
Sequence 178 BP; 0 A; 52 C; 46 G; 32 T;
Query Match 1.7%; Score 37; DB 32; Length 178;
Best Local Similarity 34.2%; Pred. No. 6.19e-06;
Matches 26; Conservative 33; Mismatches 16; Indels 1; Gaps 1;

[illegible]

Dd 102 tggcbbgcbccbbcbgbgbbbcbtbgbgbb-tbtcbcttcgtgbbbbbg 160
||||| : | : |||| : : : |||| : | : |||| : | : |||| :

Cp 137 TGGCCCGGCGCATGGCGGCGGCCGAGTTCGGGGCCTGTCTCGCGATCGTTCTCTC 78

Dd 161 ggbtccccccc 176
.:|:::|| |||

Cp 77 CCTCTCTGGCCACC 62

RESULT 7

ID RT76170 standard; DNA; 88 BP.

AC RT76170;

DT 12-SEP-1997 (first entry)

KW Human IL3 receptor antisense oligonucleotide.

DE Asthma; airway epithelium; adenosine free; cystic fibrosis;

KW chronic obstructive pulmonary disease; bronchitis; interleukin; ss.

OS Synthetic.

PN WO9640162-AI.

PD 19-DEC-1996.

Pf 06-JUN-1996; UO9306.

PR 07-JUN-1995; US-47497.

PA (UYEC-) UNIV EAST CAROLINA.

PI Metzger WJ, Nyce JW;

DR WP1; 97-051871/05.

PT Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of subject

PS Example 5; Page 28; 7lpp; English.

CC A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the CC subject. The present sequence is an antisense oligonucleotide specific for the human IL3 receptor, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma,

CC chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced CC bronchoconstriction in patients with hyper-reactive airways.

SQ Sequence 88 BP; 0 A; 22 C; 36 G; 5 T;

Query Match 1.6%; Score 35; DB 32; Length 88;
Best Local Similarity 44.6%; Pred.No.6.lle-05;
Matches 37; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

Dd 1 gcbbgbcgcbggygcgcbtgcbgcbgcbgbbgcbgcbcgcbgcbgcbgcbg 60
|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|

Cp 243 GCCGAGCGGTGCACAAGCGCGGGTGCA CGGACCCCTCGTGTGGACGCCGGCGCG 184

Dd 61 cbgctcgcgbbcgbgcbcbg 83
|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|

Cp 183 CTGCCATCTCTCTCCGAGCTGCG 161

RESULT 8

ID RT07469 standard; DNA; 114 BP.

AC RT07469;

DT 07-APR-1995 (first entry)

DE Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW effector domain; concatenated heterofunctional protein; linker;
KW direct; rapid; detection; screening; treatment; generic; ss.

OS Synthetic.

FH key Location/Qualifiers

FT misc_feature 55..60 /tag= a
FT FT /note= "this sequence represents 'Z'; Z can be a
sequence of 6,9 or 12 nucleotides (see comments)"
FN WO9418318-A.
PD 18-AUG-1994.
PF 01-FEB-1994; UO0977.

CC and Y are flanking restriction sites (X is not the same as Y) that are
CC not specified further. Other generic sequences are shown in Q70466-68.
CC Other specific peptides generated by these generic sequences are shown in
CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC comprising at least two functional regions - a binding domain with
CC affinity for a ligand and a second effector peptide portion that is
CC chemically or biologically active. They may further comprise a linker
CC peptide between the 2 domains. The oligonucleotides are also designed so
CC that the expressed peptide contains 2 or 4 cysteine residues positioned
CC in, or flanking, the unpredicted or variant residues. These residues
CC confer some degree of conformational rigidity to the peptides. The TSARs
CC or comprints, comprising a TSAR binding domain can be used in vivo to
CC deliver a chemically or biologically active moiety, eg. metal ion,
CC radioisotope, peptide, toxin or enzyme, to the specific target or on the
CC cell. They can also replace the function of macromolecules, eg.
CC monoclonal or polyclonal antibodies and therefore circumvent the need
CC for complex methods of hybridoma formation or in vivo antibody
CC production. The TSARs are easily characterised and have designed activity
CC allowing direct and rapid detection in a screening process.
SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

Query Match 1.6%; Score 34; DB 12; Length 114;
Best Local Similarity 3.7%; Pred. No. 1.89e-04;
Matches 4; Conservative 32; Mismatches 72; Indels 0; Gaps 0;

Db 3 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnnn 62

QY 200 CAGGAGGGTCCGCTGCACCGCGCTTCTGCACCGCGCTTCTGCACCGCGCGCC 259

Db 63 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnn 110

QY 260 TCCCGCTCCATGTTCTTGGCCCTCTGGGGCTGGGACTGGCCAGGTG 307

RESULT 11

ID Q70468 standard; DNA; 114 BP.
AC Q70468:
DT 05-APR-1995 (first entry)
DE Generic DNA sequence to generate a random TSAR peptide library.
KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW effector domain; concatenated heterofunctional protein; linker;
KW direct; rapid; detection; screening; treatment; generic; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 55..60
FT /*tag= a
FT /*note= "this sequence represents 'z'; z can be a
FT sequence of 6, 9 or 12 nucleotides (see
FT comments)"

W09418318-A.

PD 18-AUG-1994.
PF 01-FEB-1994; U00977.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PA (UYNC-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Kay BK;
DR WPI: 94-279739/34.
DR P-PSDB: R65154.
PT Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 35; 255pp; English.
CC Q70468 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generic formula can also be
CC represented as follows: X(NNB)11(TGC)(NNB)62(TGC)(NNB)10Y. X
CC and Y are flanking restriction sites (X is not the same as Y) that are
CC not specified further. Other generic sequences are shown in Q70466-68.
CC Other specific peptides generated by these generic sequences are shown in
CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC comprising at least two functional regions - a binding domain with
CC affinity for a ligand and a second effector peptide portion that is
CC chemically or biologically active. They may further comprise a linker

CC peptide between the 2 domains. The oligonucleotides are also designed so
CC that the expressed peptide contains 2 or 4 cysteine residues positioned
CC in, or flanking, the unpredicted or variant residues. These residues
CC confer some degree of conformational rigidity to the peptides. The TSARs
CC or comprints, comprising a TSAR binding domain can be used in vivo to
CC deliver a chemically or biologically active moiety, eg. metal ion,
CC radioisotope, peptide, toxin or enzyme, to the specific target or on the
CC cell. They can also replace the function of macromolecules, eg.
CC monoclonal or polyclonal antibodies and therefore circumvent the need
CC for complex methods of hybridoma formation or in vivo antibody
CC production. The TSARs are easily characterised and have designed activity
CC allowing direct and rapid detection in a screening process.
SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

Query Match 1.6%; Score 34; DB 12; Length 114;
Best Local Similarity 3.6%; Pred. No. 1.89e-04;
Matches 4; Conservative 33; Mismatches 75; Indels 0; Gaps 0;

Db 3 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnnn 62

QY 191 GGCCTCCACACGAGGTCCGCTGCACCGCGCTTCTGCACCGCGCTCCGCGCGCCA 250

Db 63 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnn 114

QY 251 CCCCGCGCTCCGCTCCATGTTCTGCGCCCTCTGGGGCTGGGACTGGGCC 302

RESULT 12

ID Q70467 standard; DNA; 114 BP.

AC Q70467:

DT 05-APR-1995 (first entry)

DE Generic DNA sequence to generate a random TSAR peptide library.

KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;

KW effector domain; concatenated heterofunctional protein; linker;

KW direct; rapid; detection; screening; treatment; generic; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT misc_feature 55..60

FT /*tag= a

FT /*note= "this sequence represents 'z'; z can be a

FT sequence of 6, 9 or 12 nucleotides (see

FT comments)"

W09418318-A.

PD 18-AUG-1994.
PF 01-FEB-1994; U00977.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PA (UYNC-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Kay BK;
DR WPI: 94-279739/34.
DR P-PSDB: R65153.
PT Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 35; 255pp; English.
CC Q70467 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generic formula can also be
CC represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)1Y. X
CC and Y are flanking restriction sites (X is not the same as Y) that are
CC not specified further. Other generic sequences are shown in Q70466-68.
CC Other specific peptides generated by these generic sequences are shown in
CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC comprising at least two functional regions - a binding domain with
CC affinity for a ligand and a second effector peptide portion that is
CC chemically or biologically active. They may further comprise a linker
CC peptide between the 2 domains. The oligonucleotides are also designed so
CC that the expressed peptide contains 2 or 4 cysteine residues positioned
CC in, or flanking, the unpredicted or variant residues. These residues
CC confer some degree of conformational rigidity to the peptides. The TSARs
CC or comprints, comprising a TSAR binding domain can be used in vivo to
CC deliver a chemically or biologically active moiety, eg. metal ion,
CC radioisotope, peptide, toxin or enzyme, to the specific target or on the

[illegible][illegible]

CCP
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RESULT 14

ID Q70463 standard; DNA; 114 BP.
AC Q70465:

DI 03-APR-1993 (first entry)
DE Generic DNA sequence to generate a random TSAP netide library

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effect domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
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FT      /*tag=      a
FT      /note= "this sequence represents '2'; 2 can be a
FT      sequence of 6, 9 or 12 nucleotides (see
FT      comments)"
FT
FT      W09418318-A.
PD      18-AUG-1994.
PE      01-FEB-1994; U00977.
PPR      01-FEB-1993; US-013416.
PPR      30-DEC-1993; US-176500.
PPR      31-JAN-1994; US-189331.
PPA      (UYNC-) UNIV NORTH CAROLINA.

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PI Folkes DM, Kay BK;
 DR WPI; 94-279739/34.
 DR P-PSDB; R65150 and R65151.
 DR Identifying proteins or peptide(s) which bind a ligand - by
 DR screening a recombinant vector library expressing fusion proteins
 PT comprising a binding domain and an effector domain
 PT
 PS Disclosure: Page 35; 253pp; English.
 PS Q70465 is a generic DNA sequence used to generate random TSAR (Totally
 CC Synthetic Affinity Reagents) peptides.This generic formula can also be
 CC represented as follows: X(NNB)6(TGC)(NNB)11z(NNB)14(TGC)(NNB)3Y. X
 CC and Y are flanking restriction sites (X is not the same as Y) that are
 CC not specified further. Other generic sequences are shown in Q70466-68.
 CC Other specific peptides generated by these generic sequences are shown in
 CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides
 CC comprising at least two functional regions - a binding domain with
 CC affinity for a ligand and a second effector peptide portion that is
 CC chemically or biologically active.They may further comprise a linker
 CC peptide between the 2 domains.The oligonucleotides are also designed so
 CC that the expressed peptide contains 2 or 4 cysteine residues positioned
 CC in, or flanking, the unpredicted or variant residues. These residues
 CC confer some degree of conformational rigidity to the peptides. The TSARs
 CC or compsns, comprising a TSAR binding domain can be used in vivo to
 CC deliver a chemically or biologically active moiety, eg. metal ion,
 CC radioisotope, peptide, toxin or enzyme, to the specific target or on the
 CC cell. They can also replace the function of macromolecules, eg.
 CC monoclonal or polyclonal antibodies and therefore circumvent the need
 CC for complex methods of hybridoma formation or in vivo antibody
 CC production. The TSARs are easily characterised and have designed
 CC activity allowing direct and rapid detection in a screening process.
 CC Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
 SQ

Query Match 1.6%; Score 34; DB 12; Length 114;
 Best Local Similarity 3.6%; Pred.No. 1.89e-04;
 Matches 4; Conservative 33; Mismatches 75; Indels 0; Gaps 0
 Db 3 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnnnnn 62

[illegible]

Db 63 bnnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbtgcnnbnbnab 114
 : : : : : : : : : : : : : : : :
Cp 157 GTACTTGGCGTAGTCTGGCTGGCCGCGCATGGCGCGCGCCCGAGTTC 106

RESULT 15

ID Q70468 standard; DNA; 114 BP.

AC Q70468;

DE 05-APR-1995 (first entry)

DE Generic DNA sequence to generate a random TSAR peptide library.

DE TSAR: totally synthetic affinity reagent; synthetic; binding domain;

DE KW effector domain; concatenated heterofunctional protein; linker;

DE KW direct; rapid; detection; screening; generic; ss.

OS Synthetic.

OS Key

OS Location/Qualifiers

FT misc_feature 55..60

FT /*tag= a

FT /note= "this sequence represents 'z'; z can be a

FT sequence of 6, 9 or 12 nucleotides (see

FT comments)"

W09418318-A.

PD 18-AUG-1994.

PD 01-FEB-1994. U00977.

PD 01-FEB-1993; US-013416.

PR 30-DEC-1993; US-176500.

PR 31-JAN-1994; US-189331.

PR (UYNC-) UNIV NORTH CAROLINA.

PI Fowlkes DM, Key BK;

PI WPI; 94-279739/34.

P-PSDB; R65154.

DR Identifying proteins or peptides(s) which bind a ligand - by

DR screening a recombinant vector library expressing fusion proteins

DR comprising a binding domain and an effector domain

DR Disclosure; Page 35; 255pp; English.

PS Q70468 is a generic DNA sequence used to generate random TSAR (Totally

CC Synthetic Affinity Reagents) peptides. This generic formula can also be

CC represented as follows: X(NNB)11(TGC)(NNB)62(NNB)7(TGC)(NNB)10Y. X

CC and Y are flanking restriction sites (X is not the same as Y) that are

CC not specified further. Other generic sequences are shown in Q70466-68.

CC Other specific peptides generated by these generic sequences are shown in

CC Q65151-54. TSARs are concatenated heterofunctional proteins or peptides,

CC comprising at least two functional regions - a binding domain with

CC affinity for a ligand and a second effector peptide portion that is

CC chemically or biologically active. They may further comprise a linker

CC peptide between the 2 domains. The oligonucleotides are also designed so

CC that the expressed peptide contains 2 or 4 cysteine residues positioned

CC in, or flanking, the unpredicted or variant residues. These residues

CC confer some degree of conformational rigidity to the peptides. The TSARs

CC or compns. comprising a TSAR binding domain can be used in vivo to

CC deliver a chemically or biologically active moiety, eg. metal ion,

CC radioisotope, peptide, toxin or enzyme, to the specific target or on the

CC cell. They can also replace the function of macromolecules, eg.

CC monoclonal or polyclonal antibodies and therefore circumvent the need

CC for complex methods of hybridoma formation or in vivo antibody

CC production. The TSARs are easily characterised and have designed activity

CC allowing direct and rapid detection in a screening process.

CC Sequence 114 BP; 2 C; 2 G; 2 T;

SQ Sequence 114 BP; 2 C; 2 G; 2 T;

	Query Match	1.6%	Score 34;	DB 12;	Length 114;
	Best Local Similarity	3.6%;	Pred.No. 1.89e-04;		
	Matches	4;	Conservative 33;	Mismatches 75;	Indels 0; Gaps 0;
Db	3 bnaabnbnbnbnbnbnbnbnbnbtgcnnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbn	62			
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	187 GC CGCTGCCCATCTCCTCCGAGTGGCGAGGTACTTCGC GTAGTTCGCTGGCCGGCG	128			
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Cp	: : : : : : : : : : : : : :	:			
	127 CATGGCGGGCGCGCCCGAGATTCGGGGCGCCCTGTGTCGCGATCGTTCTCC	76			

Search completed: Sat Nov 14 03:20:42 1998

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Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

on: Sat Nov 14 00:39:32 1998; MasPar time 2910.85 Seconds
ular output not generated. 1538.313 Million cell updates/sec

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Perfect Score: 2191
N.A. Sequence: 1 GCAGGACCTCTGTGAACG.....TTTTGGTACTTAAATGGC 2191
Comp: CGGCTCTGGAGACACTGTGC.....AAAACCATGAATTTTACCG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 552174 segs, 1021863385 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb155
1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om
7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro
Database: genbank107
12:gb_ba 13:gb_htg 14:gb_in 15:gb_om 16:gb_ov 17:gb_pat
18:gb_ph 19:gb_pl 20:gb_pr1 21:gb_pr2 22:gb_ro 23:gb_st
24:gb_sts 25:gb_sy 26:gb_un 27:gb_vi

Statistics: Mean 12.129; Variance 6.937; scale 1.749

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2152	98.2	2299	22	Mus musculus osteoprot	0.00e+00
2	2150	98.1	2235	22	Mus musculus receptor	0.00e+00
3	2070	94.5	2237	22	Mus musculus TNF-relat	0.00e+00
4	951	43.4	951	22	Mus musculus mRNA for	0.00e+00
5	848	38.7	2271	21	Homo sapiens osteoprot	0.00e+00
6	842	38.4	2201	21	Homo sapiens receptor	0.00e+00
7	715	32.6	1833	21	Homo sapiens TNF-relat	0.00e+00
8	55	2.5	10772	14	Drosophila melanogaste	6.20e-15
c 9	52	2.4	10772	14	Drosophila melanogaste	3.84e-13
10	47	2.1	7218	17	Sequence 14 from patent	3.22e-10
c 11	41	1.9	7218	17	Sequence 14 from patent	7.68e-07
c 12	39	1.8	215	17	Sequence 5 from patent	9.41e-06
13	40	1.8	74371	21	Homo sapiens chromosome	2.70e-06
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15	35	1.6	215	17	Sequence 5 from patent	1.21e-03

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c 18	1.4	4050	14	DPROXING	D.discoideum gene for	3.63e-01
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20	1.4	161708	13	AC005295	Homo sapiens thaliosom	3.10e+00
21	1.3	201	17	A10158	S.griseus gene for pre	3.10e+00
22	1.3	201	17	A10161	Synthetic DNA for prep	3.10e+00
c 23	1.3	201	17	A10159	S.griseus gene for pre	3.10e+00
c 24	1.3	201	17	A10162	Synthetic DNA for prep	3.10e+00
c 25	1.3	402	21	SOU60998	Saguinus oedipus clone	3.10e+00
c 26	1.3	421	24	G08367	human STS CHLC.GATA46B	3.10e+00
c 27	1.3	565	17	E04076	gDNA encoding envelope	3.10e+00
c 28	1.3	1265	19	DDITF1D	D.discoideum rFIID mRN	1.07e+00
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c 33	1.3	2368	17	A20297	wun1 and flanking reg	1.07e+00
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41	1.3	123520	13	AC005139	*** SEQUENCING IN PROG	1.07e+00
c 42	1.3	149316	13	AC005008	Homo sapiens clone GSO	3.10e+00
c 43	1.3	168827	13	HS616B8	Human DNA sequence ***	3.10e+00
c 44	1.3	182705	13	AC005084	Homo sapiens clone RG2	3.10e+00
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ALIGNMENTS

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LOCUS		Mus musculus osteoprotegerin ligand mRNA, complete cds.				
DEFINITION		Mus musculus osteoprotegerin ligand mRNA, complete cds.				
ACCESSION		AF053713				
NID		G3057147				
KEYWORDS		house mouse.				
SOURCE		Mus musculus				
ORGANISM		Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE		1 (bases 1 to 2299)				
AUTHORS		Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R., Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S., Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A., Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J., Delaney, J. and Boyle, W.J.				
TITLE		Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation				
JOURNAL		Cell 93 (2), 165-176 (1998)				
MEDLINE		98227661				
REFERENCE		2 (bases 1 to 2299)				
AUTHORS		Boyle, W.J.				
TITLE		Direct Submission				
JOURNAL		Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc., One Amgen Center Drive, Thousand Oaks, California 91320, USA				
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Best Local Similarity 99.5%; Pred. No. 0.00e+00;
Matches 2177; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

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Db 2204 TGAATGTTAATTTTGTGTACAAAAA 2230
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RESULT 2
LOCUS AF019048 2225 bp mRNA ROD 22-NOV-1997
DEFINITION Mus musculus receptor activator of nuclear factor kappa B ligand
          (RANKL) mRNA, complete cds.
ACCESSION AF019048
NID 92612923
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2225)
AUTHORS Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
Tometsko,M.E., Roux,E.R., Teepe,M.C., DuBose,R.F., Cosman,D. and
Galibert,L.
TITLE A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
JOURNAL Nature 390 (6656), 175-179 (1997)
MEDLINE 98032977
REFERENCE 2 (bases 1 to 2225)
AUTHORS Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E.,
Cosman,D., DuBose,R. and Galibert,L.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA
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Best Local Similarity 99.5%; Pred. No. 0.00e+00;
Matches 2176; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
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QY 1 GCCAGACACCTCTGTGAACCGGTGCGGGCGGGCGCGCTGCGCGGGAGTGTGTCGCGG 60
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QY 61 TGGGTGCGCGGAGGAGGAGACGATCGCGGAGCGGGCGCGCGCACTCCGGCGCGCG 120
Db 133 CGGCATCGCGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 192

```

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QY 121 GCCATCGCGCGGGCAGCCGAGACTACGGCAAGTACCTGCGCAGCTCGGAGGAGATGG 180
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Db 253 GCGCGCGCACCCCGCGCTCCGCTCCATGTTCTTGGCCCTCTCTGGGCTGGGACTGGG 312
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Db 313 CCAGTGTCTGCGAGCATCGCTCTCTTCTGTACTTTCGAGCGCAGATGGATCCTAACAG 372
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QY 421 TTTGAGGACTCGACTCTGGAGAGTGAAGACACACTACTCTGACTCTCTGCGAGGAGTAA 480
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LOCUS	DEFINITION	Mus musculus TNF-related ligand	TRANSE	complete cds.		
ACCESSION	NID	AF013170	g2411497			
KEYWORDS	SOURCE	house mouse.				

ORGANISM	Mus musculus
REFERENCE	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 2237) Wong,B.R., Rho,J., Arron,J., Robinson,E., Orlickick,J., Chao,M., Kalachikov,S., Cayani,E., Bartlett,F.S. III, Frankel,W.N., Lee,S.Y. and Choi,Y.
TITLE	TRANSE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells
JOURNAL	J. Biol. Chem. 272 (40), 25190-25194 (1997)
MEDLINE	97460112
REFERENCE	2 (bases 1 to 2237)
AUTHORS	Wong,B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and Choi,Y.
TITLE	Direct Submission
JOURNAL	Submitted (09-JUL-1997) Howard Hughes Medical Institute, The Rockefeller University, 1230 York Ave., New York, NY 10021, USA
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DEFINITION Mus musculus mRNA for osteoclast differentiation factor (ODF), complete cds.
ACCESSION AB008426
NID 93041781
KEYWORDS osteoclast differentiation factor (ODF).
SOURCE Mus musculus bone marrow stromal cells cell_line:ST2 cdna to mRNA, clone_lib:pCDL-Sra296 clone:pOBM291.
ORGANISM Mus musculus
Eukaryota; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Yasuda,H., Shima,N., Nakagawa,N., Yanaguchi,K., Kinoshita,M., Mochizuki,S., Tomoyasu,A., Yano,K., Goto,M., Murakami,A., Tsuda,E., Morinaga,T., Higashio,K., Udagawa,N., Takahashi,N. and Suda,T.
Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL
Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3597-3602 (1998)
JOURNAL 98188248
MEDLINE 2 (bases 1 to 951)
REFERENCE Yasuda,H.
AUTHORS Direct Submission
TITLE Submitted (22-OCT-1997) to the DDBJ/EMBL/GenBank databases.
JOURNAL Histatka Yasuda, Snow Brand Milk Products Co., Ltd., Research Institute of Life Science; 519 Shimo-Ishibashi, Iishibashi-machi, Tochihi 329-05, Japan (E-mail:fvb7042emb.infoweb.or.jp, Tel:0285-52-1331, Fax:0285-53-1314)

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DEFINITION	Homo sapiens osteoprotegerin ligand mRNA, complete cds.		
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REFERENCE	1 (bases 1 to 2271)		
AUTHORS	Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R., Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S., Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A., Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J., Delaney, J. and Boyle, W.J.		
TITLE	Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation		
JOURNAL	Cell 93 (2), 165-176 (1998)		
MEDLINE	98227661		
REFERENCE	2 (bases 1 to 2271)		
AUTHORS	Boyle, W.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc., One Amgen Center Drive, Thousand Oaks, California 91320, USA		
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QY	725	AGCAACGGAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTC	784
Db	661	TTTCGGCATCATGAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTAT	720
QY	785	TTTCGGCATCATGAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTAT	844
Db	721	GTGCTTAAACACGACATCAAAATCCCAAGTCTCATACCTGATGAAGGAGGAGGACGC	780
QY	845	GTGCTTAAACACGACATCAAAATCCCAAGTCTCATACCTGATGAAGGAGGAGGACGC	904
Db	781	AAAACTGGTGGGCAATCTGAATTCACATTTTATTCATATAATGTTGGGGGATTTTC	840
QY	905	AAAACTGGTGGGCAATCTGAATTCACATTTTATTCATATAATGTTGGGGGATTTTC	964
Db	841	AAGTCGAGCTGGTGAAGAAATAGCATTAGCTGAGTGCACACCTTCCTCTCGATCCG	900
QY	965	AAGTCGAGCTGGTGAAGAAATAGCATTAGCTGAGTGCACACCTTCCTCTCGATCCG	1024
Db	901	GATCAAGATCGGAGTACTTTGGGCTTTCAAGTTTCAAGGACATAGACTGA	951
QY	1025	GATCAAGATCGGAGTACTTTGGGCTTTCAAGTTTCAAGGACATAGACTGA	1075
RESULT	5		
LOCUS	AF053712	2271 bp mRNA	PRI 09-MAY-1998
DEFINITION	Homo sapiens osteoprotegerin ligand mRNA, complete cds.		
ACCESSION	AF053712		
NID	93057145		
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 2271)		
AUTHORS	Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R., Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S., Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A., Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J., Delaney, J. and Boyle, W.J.		
TITLE	Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation		
JOURNAL	Cell 93 (2), 165-176 (1998)		
MEDLINE	98227661		
REFERENCE	2 (bases 1 to 2271)		
AUTHORS	Boyle, W.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc., One Amgen Center Drive, Thousand Oaks, California 91320, USA		
FEATURES	Location/Qualifiers		
source	1. .2271		
	/organism="Homo sapiens"		
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	185. .1138		
CDS	/function="regulates osteoclast differentiation and activation"		
	/codon_start=1		
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	/translation="MRRASRDYTKYLRSSEEMGGPGAPHEGLHAPPPAPHPAPPA		
	SRSEFALLGLGQVVCSTVALFFYFRAQMDPNRISDTHCIYRLRLHFNADFDPT		
	TSLSDITLDCSRKQAFQAGVQKELQHVGPQFSGAPAMMGESWLDVAQRGKE		
	AQPFAHLTINAATIPSGSHKVLSSWYHGRWAKISNMTLSNGKLRVNDGDFYLYA		
	ICFRHETSGDALTLOLMVYVVKTSIKIPSSHTLMKGGSTKYWGSNGSEFPFYSIN		
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BASE COUNT	658 a	462 c	522 g 629 t
ORIGIN			
Query Match 38.7%; Score 848; DB 21; Length 2271;			
Best Local Similarity 78.5%; Pred. No. 0.00e+00;			
Matches 1642; Conservative 0; Mismatches 380; Indels 69; Gaps 43;			
Db	173	GGGCGGAGCGCATCGCGCGCCGACGAGACTACACCAAGTACCTCGGTGCGGAG	232

113 GGCGCGCGCCATGGCCGGGCGCAGCCGAGACTACGGCAAGTACCTGCGCAGCTCGGAG 172
Db 233 GAGATGGGCGCGCCCGGAGCCCGCAGAGGCGCCCTGCGACGCGCCGCGCC-6C- 290
QY 173 GAGATGGGCGCGCCCGGAGCCCGCAGAGGCGCCCTGCGACGCGCCGCGCTTCGCA 232
Db 291 -CTGCGCGCGCACCAGCGCCCGCGCGCCCTGCGATGCTGCGCGCCCTGCGCGCTG 349
QY 233 CGGCTCCGCGCGCCCGCACCAGCGCGCCCTGCGATGCTGCGCGCCCTGCGCGCTG 292
Db 350 GGGCTGGCGCGAGGTGCTGCGCGCGCGCCCTGCGATGCTGCGCGCCCTGCGCGCTG 409
QY 293 GGAATGGCGCGAGGTGCTGCGCGCGCGCCCTGCGATGCTGCGCGCCCTGCGCGCTG 352
Db 410 CTAATAGAAATATCAGAAGATGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 469
QY 353 CTAATAGAAATATCAGAAGATGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 412
Db 470 AATGCGAGATTTTCAAGACACAACTCTGAGAGTCAAGATACAAATTAATACCTGATTCA 529
QY 413 AAGCGAGTTTGCAGGACTGACTCTGGAGAGTGAAGACACAC-----TACCTGACTCC 466
Db 530 TGTAGGAGATTTAAGAGCGCTTCAAGGAGCTGTGCAAGGAAATTAACACATATCGTT 589
QY 467 TGCAGGAGGATGAACAAGCGCTTCAAGGAGCGCTGCGAGGAACTGCAACATTTGTG 526
Db 590 GATACACAGCATCAGACAGAGAAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
QY 527 GGGCCACAGCGCTTCTCAGAGGCTCCAGCTATGATGGAAGGCTCATGTTGGATGTGGCC 586
Db 650 AAGAGGAGCAAGCTTGAAGCTCAGCGCTTTTTCATCTCCTGCTGCTGCTGCTGCTGCTG 709
QY 587 CAGCGAGGCAAGCGCTGAGGCGCCAGCGCTTTCACACCTCACCATCAATGCTGCGCAGATC 646
Db 710 CCATCTGGTTCCCATAAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
QY 647 CCATCGGTTCCCATAAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 706
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QY 707 ATCTCAACATGACTTTAGCAATGGAAGAACTAATAGTTAATCAGGATGCTTTTATAC 766
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QY 767 CTGTATGCCAACATTTGCTTTGACATCATGAACCTTCAGGAGCTGCTGCTGCTGCTGCTG 826
Db 890 CTTCACATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 949
QY 827 CTTCACATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 886
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QY 947 AATGTTGGGGGATTTTCAAGCTCCGAGCTGCTGAGGAAATTAGCAATTCAGGCTGCCAAC 1006
Db 1070 CCTCTCTACTGATCGGATCGGATGAGGATGCAACATCTTTGGGCTTTTAAAGTTCAGAT 1129
QY 1007 CCTCTCTCTGATCGGATCGGATGAGGATGCAACATCTTTGGGCTTTTAAAGTTCAGAT 1066
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QY 1067 ATAGATTGAGCCCGCTTTTGGAGTCTTA--TGTATTTCTGGGATTTTGGAAACATT 1124
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QY 1125 TCTTAAAGATG---GAT-GATGCTATACATGCTGTAAGCACTTAAGACATGCGCC 1179
Db 1247 CAAAGGTACAGCACTCAGTATCCAGTCTTGGACCTTTGATAGAGAACACGCGTATTTACAG 1306
QY 1180 ACGGTGTATGAAGCACTCAGACCCCTCTCTCTGAGCCTGTACAGGTTGTGTATATGTAAG 1239

Db 1307 CCAGTGGGAGATGTTAGACTCATGCTGCTGTACACAATGGTTTAAATTTTGTATGAA 1366
QY 1240 TCCATAGGTGATGTTAGATTATCATGTGA-TTACAACAGGTTTACAATTTTGTATGAT 1298
Db 1367 TTCTTA-GAATTAACACAGATTGG---AGCAATTAACGG-G--T-TGAC---CTTATGAGA 1415
QY 1299 TTCTTAAGAATTAACACAGATTGGGAGAGGATTTCCGATGCTTATGAAAACCTTACACGT 1358
Db 1416 AA-CT--GCATGTGGGCTATGGAG--GGGT-TGTCCTTGTGCTATGTCCTTCCGACG 1469
QY 1359 GAGCTATGGAAGGGGTCACAGTCTCTGGTCTAAACCTGACATGTCCTGAGAAC 1418
Db 1470 CT-GAAGTGGAGAGGGTGTCACT-AGCGCAATTCAGAGATCATCTGAAGGGGCAAAATTC 1527
QY 1419 CTTGAATTAAGAAGATGCCATGTCATTGCAAGAAATGATAGTGTGAAGGGTTAGTTTC 1478
Db 1528 TTTTGAATTTTACATCATGCTGGAACCTGCAAAAAA-TACTTTTT--CTAATGAGGAGA 1584
QY 1479 TTTTGAATTTTACATCATGCTGGAACCTGCAAAAAA-TACTTTTT--CTAATGAGGAGA 1538
Db 1585 GAAAA-TATATGATTTTAT 1643
QY 1539 GAAAA-TATATGATTTTAT 1598
Db 1644 TGAAGATTTTAAATTTAT 1703
QY 1599 TGAAGATTTTAAATTTAT 1658
Db 1704 CTTGCTGTTGACATATTTAATGTTTAAATTTAATGTTACAGATATATTTAACGCTGCTGCT 1763
QY 1659 CTTGCTGTTGACATATTTAATGTTTAAATTTAATGTTACAGATATATTTAACGCTGCTGCT 1718
Db 1764 AAATTCCTGGGAAACCTGACGCTAGGAGGGGAAAAAATGTTGT-TCCATATATAT 1822
QY 1719 AATTCCTGGAGGTA-CTCGTAGCTAGGAGGGGAGATATCTGTTCTGGTGACCACTG 1777
Db 1823 AAATGCACTA-TAT-TTCTTCTGTT-CTTTTAA-AGTTAATAGATTTTTCAGACATTTGCA 1878
QY 1778 TAGTTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1837
Db 1879 AGCTG-TGCA--AA-AAAAATTAATGATGCTTGAATTAATAGCAGGATTTGGCCA 1934
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Db 1935 CCAGTGGCTTTCAAAATTTAGAACTAATGACCTTTAGAACTGACATTTGCCAAAAGG 1994
QY 1938 CCAGTGGCTTTCAAAATTTAGAACTAATGACCTTTAGAACTGACATTTGCCAAAAGG 1956
Db 1995 ATACATATGGCCCACTGAAA-TCTGTCAAGAGTAGTTATATATATTTGTGAACAGGTG- 2052
QY 1957 ATACATATAGGCTACTGAAAATCTGTCAGGAGTATTTATGCAATTTATGACAGGTGTC 2016
Db 2053 -TTTCCACAGTGGCGCAATTTGACCTTTT-TT-TTTTTCACAAATAGAAAAGTTA 2108
QY 2017 TTTTTCACAGAGCTACAAATTTGAAATTTTGTCTTTTCTTTTCTTTTCTTTTCTTTTCT 2076
Db 2109 TTAGTGGTTTATCAGC--AAAA-AGTCCAATTT-AAATTTAGTAAATGTTATCTTAT-- 2162
QY 2077 CTA-TAGTTTATCAGCCAAAAACAATCCACTTTTAAATTTAGTGAAGTTTATTTATTA 2135
Db 2163 -ACTGTACATAAAAAACATTCCTTTGAATGTTAATTTTGGTACAAAA 2212
QY 2136 TACGTACATAAAGCAATTTCTGTAAGGCA-TTTTGTGGTACTTAA 2185

RESULT 6

LOCUS

AF019047 2201 bp mRNA

PRI

22-NOV-1997

DEFINITION

Homo sapiens receptor activator of nuclear factor kappa B ligand
(RANKL) mRNA, complete cds.

ACCESSION

AF019047

NID

g2612921

KEYWORDS

n

Db 838 GCATGCCCAACG-GTACACGACTCAGTATCCATCTCTTGACCTTGTAGAGAACACGCG 896
QY 1171 ACATGCCCAACGCTGTATGAATCTACAGCCCTCTCTTGAGCCTGTACAGGTGTGTA 1230
Db 897 TATTACAGCCAGTGGGAGATGTAGACTCATGGTGTGTACAAATGCGTTTAAATTT 956
QY 1231 TATGTAAGTCCATAGTGTATGTATTCATGTGTA-TTACACACGGTTTACAAATTT 1289
Db 957 TGAATGAATTCCTA-GAATTAACACAGATGG---AGCAATTACGG-G-TTGAC--- 1005
QY 1290 TGAATGAATTCCTAAGAATTAACACAGATGGAGAGAGTATCCGATGCTTATGAATA 1349
Db 1006 CTTATGAGAA-CT--GCATGTGGCTATGGAG--GGGT-TGCTCCCTGTCATGCGC 1059
QY 1350 CTTACAGCTGAGCTATGGAAGGGGTACAGTCTCTGCGGTCTAACCCCTGGACATGCGC 1409
Db 1060 CTTCCGAGCT-GAAGTGGAGAGGGTGTCACT-AGCGCAATTGAAGGATCACTGAAGG 1117
QY 1410 ACTGAGAACCTTGAAATTAGAGATGCCATGTCTATGCAAGAAATGATGTGAAGG 1469
Db 1118 GCGAAATCTTTTGAATGTGTACATCATGCTGGAACCTGCAAAAA-TACTTTT--CTA 1174
QY 1470 GTTAAGTCTTTTGAATGTGTACATTCGCTGGGACCTGCAATAAGTCTTTTTTCTA 1529
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QY 1590 TGTTTTCTGTGCAAGTTTGTAAATATATTTTGTGCTATAGTATTTGATTCAAAATATT 1649
Db 1294 TAAAAATGCTGCTGTGTGACATATTAATGTTTTTAATGTACAGACATATTTAACTGGT 1353
QY 1650 TAAAAATGCTGCTGCTGTGACATATTAATGTTTTTAATGTACAGATGTTTAACTGGT 1709
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QY 1710 GCATTTGTAATTCCTCGGGAAACTTCGAGCTAAGAGGGGAAAAAATGTTTTC 1768
Db 1414 TA-ATATCAATGCGAGTA-TAT-TTCTTCGTT-CTTTTAA-AGTTAATAGATTTTCA 1467
QY 1769 GACCACATGATGTTTATTTCTTATCTTTTAACTTAAATAGAGCTTTCAGACTTGCAA 1828
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QY 1829 AACTATCAAGCAATAATAATAATAATAATAATAATAATAATAATAATAATAAGTAGA 1888
Db 1524 TGTTGGCCACAGTGCGCTTTCAAAATTTAGAACTAATGACTTTAGAAAGCTGACATG 1583
QY 1889 TGTTGGTCACAGTGCGCTTTCAAAATTTAGAACTAATGACTTTAGGA-GCTGACATAG 1947
Db 1584 CCAAAAGGATACATAATGGCCCACTGAAA-TCTGTCAAGAGTAGTTATATATTTGTA 1642
QY 1948 CCAAAAGGATACATAATAGGCTACTGAAAATCTGTGAGGAGTATTTATGCAATTTATGA 2007
Db 1643 ACAGGTCT--TTTTCACAAAGTCGCGCAAAATTTGACCTTTT-TTGTGTTTTTCAAAATA 1699
QY 2008 ACAGGTCTTTTTCACAGAGCTACAAATTTGTAATTTGTTCTTTTTTCCCAT 2067
Db 1700 GAAAAGTATTAGTGGTTTATCAGC--AAAAA-AGTCCAAATTTT-AAATTTAGTAAATGTT 1755
QY 2068 GAAAATGTACTA-TAGTTTATCAGCAAAAAAACAATCCACTTTTAAATTTAGTGAAGTT 2126
Db 1756 ATCTTAT--ACTGTACAATAAAACATTCGCTTTGTAATTTTATTTTGGTAC 1807
QY 2127 ATTTTATTAATTAATAAAGCAATGTTTCTGTAATGCA-TTTTTTGGTAC 2180

RESULT 8
LOCUS AF012089 10772 bp DNA INV 05-AUG-1997
DEFINITION Drosophila melanogaster cysteine proteinase-1 (Cp1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds.

AF012089
92305220
fruit fly.
Drosophila melanogaster
Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Gray, Y.H., Tanaka, M.M. and Sved, J.A.
1 (bases 4546 to 4553)
p-element-induced recombination in Drosophila melanogaster: hybrid
element insertion
Genetics 144 (4), 1601-1610 (1996)
97132596
2 (bases 1 to 10772)
Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Structure of the cysteine proteinase (Cp1) gene of Drosophila
melanogaster and associated mutational effects
Unpublished
3 (bases 1 to 10772)
Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences, University
of Sydney, Biology A12, Sydney University, NSW 2006, Australia
Location/Qualifiers
1..10772
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
join(872..1000,2310..2426,6476..6690,6751..7707)
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1001..2309
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2310..2426
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HFRKSGVLVSLBQNLVDCSTKYNGNCGGLMDNAPRYIKDNGIDIEKSYPYEAD
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REFERENCE	1 (bases 1 to 7218)				
AUTHORS	Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.				
TITLE	Recombinant fowlpox virus				
JOURNAL	Patent: US 5670367-A 14 23-SEP-1997;				
FEATURES	Location/Qualifiers				
source	1.. 7218				
BASE COUNT	1944 a 1491 c 1486 g 1929 t 368 others				
ORIGIN					
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Query Match	2.1% Score 47; DB 17; Length 7218;				
Best Local Similarity	7.9%; Pred.No. 3.22e-10;				
Matches	14; Conservative 98; Mismatches 65; Indels 0; Gaps 0;				
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Db	1045	GCAGGTCCAGGAGCTGCCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1104			
Qy	162	CGAGTCGGAGGATGGCAGCGCCGCGCTCCCACAGAGGTCGCTGCACCCG 221			
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Db	1105	YYY 1164			
Qy	222	CGCCTTCTGCACGGCTCCGCGCGCCAGCCGCGCTCCCGCTCATGTTCTCTGCCCC 281			
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Qy	282	TCTTGCGGCTGGGACTGGCGCAGGTGCTGTCAGCATCGCTGTTCCTGTAATTTC 338			
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RESULT 11					
LOCUS	166494	7218 bp	DNA	PAT	23-DEC-1997
DEFINITION	Sequence 14 from patent US 5670367.				
ACCESSION	166494				
NID	g2724471				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 7218)				
AUTHORS	Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.				
TITLE	Recombinant fowlpox virus				
JOURNAL	Patent: US 5670367-A 14 23-SEP-1997;				
FEATURES	Location/Qualifiers				
source	1.. 7218				
BASE COUNT	1944 a 1491 c 1486 g 1929 t 368 others				
ORIGIN					
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Query Match	1.9% Score 41; DB 17; Length 7218;				
Best Local Similarity	0.5%; Pred.No. 7.68e-07;				
Matches	1; Conservative 113; Mismatches 73; Indels 0; Gaps 0;				
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Cp	2012	CCTGTCCAATAATGCATAAATCTCCTGCAGATTTTCAGTAGCCTATATGATATCCTT 1953			
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Db	1309	YYY 1368			
Cp	1952	TTTGCTATGTCAGCTCCTAAAGTCAATTAGCTCTAAATTTGAAGGACCTGGTGACC 1893			
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Db	1369	YYY 1428			
Cp	1892	AACATCTACTATTATTCAGATATTCATTTATTTATTTATTTATTTATTTATTTATTTGCTTGCA 1833			
Db	1429	YYYYYG 1435			
Cp	1832	AGTTTTG 1826			
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RESULT 12					
LOCUS	128278	215 bp	DNA	PAT	30-OCT-1996
DEFINITION	Sequence 5 from patent US 53569830.				
ACCESSION	128278				
NID	g1819054				
KEYWORDS	Unknown.				

SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
TITLE	Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
JOURNAL	Patent: US 5569830-A 5 29-OCT-1996;
FEATURES	Location/Qualifiers source 1..215
BASE COUNT	15 a 8 c 25 g 26 t 141 others
ORIGIN	/organism="unknown"
Query Match	1.8%; Score 39; DB 17; Length 215;
Best Local Similarity	12.5%; Pred.No. 9.41e-06;
Matches	26; Conservative 85; Mismatches 96; Indels 1; Gaps 1
Db	8 SSSVSRASCNDKAKKDGNHTTSSWTTDCCNRTWGVCDDTTYRVNNSDGHNKYSYANN 67 :: : :: : :: : :: : :: : :: : :: : :: : :: :
Cp	385 GCAGTGAGTGCCTGTCATATTCTGTGGTAGCATCCACTCGCCTCGAAAGTACAGGA 326 :: : :: : :: : :: : :: : :: : :: : :: : :: :
Db	68 YGNNVCAAKTHYYTNHVSAGDSKVTDSYNASGTSSNGGTDRSGADSGSKSTAM 127 : : : : : : : : : : : : : : : : : : : : : : :
Cp	325 CAGAGCAGTGTGCAGACCACCTGGGCCAGTCCAGCCCAGGAGGCGCCAGAACATGGA 266 : : : : : : : : : : : : : : : : : : : : : : :
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Db	187 SNVSNNCGGKNKRVDYSSYANKKCSC 214 : : : : : : : : : : : : : : : : : : : : : : :
Cp	205 CTCGTGGGACGCCGGGCGCGTGC 178
RESULT	13
LOCUS	AC005369 74371 bp DNA PRI 01-AUG-1998
DEFINITION	Homo sapiens chromosome 5, BAC clone 119j3 (LBNL HI75), complete sequence.
ACCESSION	AC005369
NID	HTG.
KEYWORDS	g3367505
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 74371) Kimmyer,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H. Sequencing of human chromosome 5 Unpublished 2. (bases 1 to 74371) Ricke,D.O. Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System Unpublished 3. (bases 1 to 74371) Kimmyer,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Davis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H. Direct Submission Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A. Sequence submitted by: DOE Joint Genome Institute. Location/Qualifiers source 1..74371 /organism="Homo sapiens" /db_xref="taxon:9606" /map="5q" /Clone="119j3"
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	


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/note="65% & 69% protein identity GenPept:U22377"
3431. .3724
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repeat_region
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/note="(A)22"
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5327. .5602
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6586. .6956
/rpt_family="L1"
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6647. .6684
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7113. .7373
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12365. .12645
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13727. .13750
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16671. .16690
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complement(16993. .17085)
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21736. .22035
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22017. .22038
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22321. .22457
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23022. .23326
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23473. .23761
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23744. .23767
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complement(25349. .25713)
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27191. .27477
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27774. .28057
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28040. .28066
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28987. .29214
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29495. .29976
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complement(30682. .30733)
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32388. .32488
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32617. .32908
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32977. .33088
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complement(33670. .33785)
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repeat_region
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QY 136 CAGCCGAGACTACGGCAAGTACCTGCGCAGCTCGGAGGAGATGGGCGGCCCGCGGT 195
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